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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:00 ; Search time 122.151 Seconds
(without alignments)
804.673 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRYFSTAVSRGRGEP.....QRYTCHVQHEGLPQLILRW 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_238Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	274	100.0	274	4	AAG64618	Aag64618 Human can
2	274	100.0	274	7	ADP55588	Adp55588 Fragment
3	274	100.0	362	4	AAG64617	Aag64617 Human can
4	274	100.0	362	4	ABP50296	Abp50296 HLA-Cw ov
5	274	100.0	362	7	ADP55587	Adp55587 Human can
6	274	100.0	362	8	ADJ75372	Adj75372 Marker ge
7	274	100.0	362	8	ADP12500	Adp12500 Protein e
8	274	100.0	442	7	ADJ70081	Adj70081 Human hea
9	250	91.2	677	4	ABG26726	Abg26726 Novel hum
10	241	88.0	271	3	AAB43986	Aab43986 Human can
11	215	78.5	215	4	AG64619	Ag64619 Human can
12	215	78.5	215	7	ADP55589	Adp55589 Fragment
13	99	36.1	120	3	AG00209	Ag00209 Human sec
14	70	25.5	186	5	ABF42931	Abf42931 Human ova
15	68	24.8	96	8	ABO57084	Ab057084 Human gen
16	44	16.1	77	8	ABO60639	Ab060639 Human gen
17	44	16.1	91	8	ABO57455	Ab057455 Human gen
18	44	16.1	104	3	AAB58497	Aab58497 Lung canc
19	44	16.1	274	1	APB0911	Apb0911 Consensus
20	44	16.1	365	8	ADP12521	Adp12521 Protein e
21	44	16.1	366	2	ARL12466	Ar12466 HLA-C exo
22	44	16.1	366	2	AXY07033	Axy07033 Breast ca
23	44	16.1	366	7	ADL62997	Adl62997 Human apo
24	44	16.1	366	7	ADP65326	Adp65326 Human HLA
25	44	16.1	366	7	ADP65316	Adp65316 Human hla

26	44	16.1	374	4	AAO13073	Aao13073 Human pol
27	44	16.1	380	4	AAU32883	Aau32883 Novel hum
28	43	15.7	120	4	AAB90793	Aab90793 Human she
29	43	15.7	130	5	ADI80341	Adi80341 Human leu
30	43	15.7	362	7	ADE31177	Ade31177 Human dia
31	40	14.6	78	8	ABO57118	Ab057118 Human gen
32	40	14.6	187	8	ADP29434	Adp29434 Human sec
33	40	14.6	314	8	ADF69311	Adf69311 Human lun
34	40	14.6	371	5	ADH48788	Adh48788 NOV31 pro
35	40	14.6	371	7	ADE40250	Ade40250 Human NOV
36	39	14.2	91	4	AAU18379	Aau18379 Peptide #
37	39	14.2	91	4	ABB37410	Abb37410 Peptide #
38	39	14.2	91	4	AAU30858	Aau30858 Peptide #
39	39	14.2	91	4	ABB32163	Abb32163 Peptide #
40	39	14.2	91	4	ABB22707	Abb22707 Protein #
41	39	14.2	91	4	AAU70538	Aau70538 Human bon
42	39	14.2	91	4	AAU58091	Aau58091 Human bra
43	39	14.2	91	4	ABG52217	Abg52217 Human liv
44	39	14.2	91	4	AAU05976	Aau05976 Peptide #
45	39	14.2	91	5	ABG40192	Abg40192 Human pep

ALIGNMENTS

RESULT 1
AAG64618
ID AAG64618 standard; protein; 274 AA.
XX AC AAG64618;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 5.
XX KW HLA-F antigen; cancer cell specific; human.
XX OS Homo sapiens.
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI: 2001-360493/38.
XX DR N-PSDB; AAH45556.
XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX PS Claim 2; Page 10-11; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX SQ Sequence 274 AA;

Query Match 100.0%; Score 274; DB 4; Length 274;

Best Local Similarity 100.0%; Pred. No. 7.5e-250;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGRGEPRIAYEVDDTQFLRFDSDAAIPRMBPREFWQEGPQYW 60

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Db 1 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAKANAQTDVALRNLRRYNSAGSHTLQMGNGCDMGPDGRLRLRYLNGKETLQ 120
Db 61 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAKANAQTDVALRNLRRYNSAGSHTLQMGNGCDMGPDGRLRLRYLNGKETLQ 120
Db 121 KYISLNEDLSRWTAAQTVAQITQRYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Qy 121 KYISLNEDLSRWTAAQTVAQITQRYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Db 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Qy 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 241 FQKWAAVVPSGEEQRYTCHVQHEGLPOPLILRW 274
Qy 241 FQKWAAVVPSGEEQRYTCHVQHEGLPOPLILRW 274
Db 241 FQKWAAVVPSGEEQRYTCHVQHEGLPOPLILRW 274

RESULT 2
ADF55588
ID ADF55588 standard; protein; 274 AA.
XX AC ADF55588;
XX DT 12-FEB-2004 (first entry)
XX DE Fragment #1 of human cancer-cell specific HLA-F antigen.
XX KW Cancer; human leukocyte antigen-F; HLA-F;
XX KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
XX KW major histocompatibility complex; MHC; cancer cell; human.
XX OS Homo sapiens.
XX PN JP2003012544-A.
XX PD 15-JAN-2003.
XX PF 27-MAR-2002; 2002JP-00088991.
XX PR 27-MAR-2001; 2001JP-00090121.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA Y.
XX DR WPI; 2003-486263/46.
XX DR N-FSDB; ADF55585.
XX PT Agent for preventing and treating cancer, comprising human leukocyte
XX antigen-F DNA, or a plasmid or viral vector comprising the DNA.
XX PS Claim 7; SEQ ID NO 5; 19pp; Japanese.
XX CC The present invention relates to an agent for preventing or treating
XX cancer. The agent comprises a portion or a complete sequence of a human
XX leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
XX presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
XX a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
XX (CTL) inducer which induces CTL which is non-specific to an organ, is
XX unrestricted to the major histocompatibility complex (MHC) and specific
XX to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
XX is useful for treating or preventing cancer. A cell capable of presenting
XX a cancer-cell specific antigen is useful for measuring HLA-F antigen and
XX for diagnosing cancer. The present sequence represents part of the human
XX cancer-cell specific HLA-F antigen.
SQ Sequence 274 AA;
Query Match 100.0%; Score 274; DB 7; Length 274;
Best Local Similarity 100.0%; Pred. No. 7.5e-250;
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81

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Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Db 1 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Qy 61 EWTGAKANAQTDVALRNLRRYNSAGSHTLQMGNGCDMGPDGRLRLRYLNGKETLQ 120
Db 61 EWTGAKANAQTDVALRNLRRYNSAGSHTLQMGNGCDMGPDGRLRLRYLNGKETLQ 120
Qy 121 KYISLNEDLSRWTAAQTVAQITQRYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Db 121 KYISLNEDLSRWTAAQTVAQITQRYEAEYAEFPRTYLEGECLELLRRYLENGKETLQ 180
Qy 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 181 RADPPKAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Qy 241 FQKWAAVVPSGEEQRYTCHVQHEGLPOPLILRW 274
Db 241 FQKWAAVVPSGEEQRYTCHVQHEGLPOPLILRW 274

RESULT 3
AAG64617
ID AAG64617 standard; protein; 362 AA.
XX AC AAG64617;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen SEQ ID 4.
XX KW HLA-F antigen; cancer cell specific; human.
XX OS Homo sapiens.
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI; 2001-360493/38.
XX DR N-FSDB; AAG45555.
XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX PS Disclosure; Page 9-10; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The
XX invention includes DNA encoding the antigen, and a method for the
XX preparation of the cancer cell specific HLA-F antigen. The antigen may be
XX used in a method to diagnose cancer, in which the protein is used to
XX detect anti-HLA-F antibodies in bodily fluids of the patient. The present
XX sequence represents the cancer cell-specific HLA-F antigen of the
XX invention.
SQ Sequence 362 AA;
Query Match 100.0%; Score 274; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 9.4e-250;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
Db 22 GSHSLRYFSTAVSRPGRGEPYIAVYDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81

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QY 61 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLRLRGYHQAIDG 120
 DB 82 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLRLRGYHQAIDG 141
 QY 121 KYIISLNEDLRSWTAADTVAQITQRFYEAEBYAEFFTYLEGECELELLRRLYENGKETLQ 180
 DB 142 KYIISLNEDLRSWTAADTVAQITQRFYEAEBYAEFFTYLEGECELELLRRLYENGKETLQ 201
 QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGT 240
 DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGT 261
 QY 241 FQKAAVVPVSGEQRVYCHVQHEGLPQPLILRW 274
 DB 262 FQKAAVVPVSGEQRVYCHVQHEGLPQPLILRW 295

RESULT 4

ABB50296
 ID ABB50296 standard; protein; 362 AA.

XX AC ABB50296;

XX DT 08-FEB-2002 (first entry)

XX DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

XX KW Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW undifferentiated carcinoma; borderline mucinous tumour; endometrioid carcinoma;
 KW adenofibroma; Brenner tumour; clear cell adenocarcinoma; cystadenofibroma;
 KW immune response pathway; serial analysis of gene expression; SAGE;
 KW membrane localised; secreted; therapeutic target; cytosolic;
 KW gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200175177-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010947.

XX PR 03-APR-2000; 2000US-0194336P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX DR WPI; 2001-626450/72.

XX DR N-PSDB; ABA83122.

XX PT Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.

XX FS Claim 23; Page 126-127; 140pp; English.

XX CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumours in an individual via the detection and measurement of the
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumour in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer, and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.

CC The methods can additionally be used to identify a particular tumour as
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma,
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumour. The ovarian tumour marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumour cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumour marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
 CC proteins encoded by ovarian tumour marker genes of the invention

XX SQ Sequence 362 AA;

Query Match 100.0%; Score 274; DB 4; Length 362;

Best Local Similarity 100.0%; Pred. No. 9.4e-250;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGEGERYIAVEYVDDTQFLRPSDAAIPRMEPREPWVEQGPQYW 60

DB 22 GSHSLRYFSTAVSRPGEGERYIAVEYVDDTQFLRPSDAAIPRMEPREPWVEQGPQYW 81

QY 61 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLRLRGYHQAIDG 120

DB 82 EWTGYAKANAQTDVVALNLLRRYNOSEAGSHTLQGNMGCDMPDGLRLRGYHQAIDG 141

QY 121 KYIISLNEDLRSWTAADTVAQITQRFYEAEBYAEFFTYLEGECELELLRRLYENGKETLQ 180

DB 142 KYIISLNEDLRSWTAADTVAQITQRFYEAEBYAEFFTYLEGECELELLRRLYENGKETLQ 201

QY 181 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGT 240

DB 202 RADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAGDGT 261

QY 241 FQKAAVVPVSGEQRVYCHVQHEGLPQPLILRW 274

DB 262 FQKAAVVPVSGEQRVYCHVQHEGLPQPLILRW 295

RESULT 5

ADF55587

ID ADF55587 standard; protein; 362 AA.

XX AC ADF55587;

XX DT 12-FEB-2004 (first entry)

XX DE Human cancer-cell specific HLA-F antigen.

XX KW Cancer; human leukocyte antigen-F; HLA-F;

XX KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;

XX KW major histocompatibility complex, WHC; cancer cell; human.

XX OS Homo sapiens.

XX PN JP2003012544-A.

XX PD 15-JAN-2003.

XX PF 27-MAR-2002; 2002JP-00088991.

XX PR 27-MAR-2001; 2001JP-00090121.

XX PA (EGAW/) EGAWA K.

XX PA (MEDI-) MEDINET KK.

XX PA (KIMU/) KIMURA Y.

DR WPI; 2003-486263/46.
 DR N-PSDB; ADF55584.
 XX
 PT Agent for preventing and treating cancer, comprising human leukocyte
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 XX
 PS Claim 5; SEQ ID NO 4; 19pp; Japanese.
 XX
 CC The present invention relates to an agent for preventing or treating
 CC cancer. The agent comprises a portion or a complete sequence of a human
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is
 CC unrestricted to the major histocompatibility complex (MHC) and specific
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
 CC is useful for treating or preventing cancer. A cell capable of presenting
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
 CC for diagnosing cancer. The present sequence represents human cancer-cell
 CC specific HLA-F antigen.
 XX
 SQ Sequence 362 AA;

Query Match 100.0%; Score 274; DB 7; Length 362;
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
 DB 22 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81
 QY 61 EWTGKAKAQTDRVALRNLRRYNOSEAGSHTLQMGCDGPDGLRLRGYHAYDG 120
 DB 82 EWTGKAKAQTDRVALRNLRRYNOSEAGSHTLQMGCDGPDGLRLRGYHAYDG 141
 QY 121 KDYISLNEEDLRSWTAADTVAQITQCFYEAEEYAEFEPTYLEGECLELLRRLYENGKETLQ 180
 DB 142 KDYISLNEEDLRSWTAADTVAQITQCFYEAEEYAEFEPTYLEGECLELLRRLYENGKETLQ 201
 QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEOTQDTVELTRPAGDGT 240
 DB 202 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEOTQDTVELTRPAGDGT 261
 QY 241 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 274
 DB 262 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 295

RESULT 6
 ADJ75372
 ID ADJ75372 standard; protein; 362 AA.
 XX
 AC ADJ75372;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:624.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EPI394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX

(GENO-) GENOX RES INC.
 Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
 WPI; 2004-193155/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Example 11; SEQ ID NO 624; 241pp; English.

CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

Sequence 362 AA;
 Query Match 100.0%; Score 274; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 60
 DB 22 GSHSLRYFSTAVSRPGGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQGPQYW 81
 QY 61 EWTGKAKAQTDRVALRNLRRYNOSEAGSHTLQMGCDGPDGLRLRGYHAYDG 120
 DB 82 EWTGKAKAQTDRVALRNLRRYNOSEAGSHTLQMGCDGPDGLRLRGYHAYDG 141
 QY 121 KDYISLNEEDLRSWTAADTVAQITQCFYEAEEYAEFEPTYLEGECLELLRRLYENGKETLQ 180
 DB 142 KDYISLNEEDLRSWTAADTVAQITQCFYEAEEYAEFEPTYLEGECLELLRRLYENGKETLQ 201
 QY 181 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEOTQDTVELTRPAGDGT 240
 DB 202 RADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEOTQDTVELTRPAGDGT 261
 QY 241 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 274
 DB 262 FQKAAVVPVSGEQRVYTCVQHEGLPQPLILRW 295
 RESULT 7
 ADP12500
 ID ADP12500 standard; protein; 362 AA.

XX AC ADP12500;
 XX DT 12-AUG-2004 (first entry)
 XX DE Protein encoded by mRNA of the invention #110.
 XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX OS Homo sapiens.
 XX PN WO2004042346-A2.
 XX PD 21-MAY-2004.
 XX PF 24-APR-2003; 2003WO-US012946.
 XX PR 24-APR-2002; 2002US-00131831.
 XX PR 20-DEC-2002; 2002US-00325899.
 XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 XX PI Rosenberg S;
 XX DR WPI; 2004-400724/37.
 XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 XX PT rejection, in an individual, comprises detecting the expression level of
 XX PT the genes.
 XX PS Claim 65; SEQ ID NO 2509; 1762pp; English.
 XX CC The present invention relates to diagnosing or monitoring transplant
 XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 XX CC comprising detecting the expression level of one or more genes. The
 XX CC methods, system and kits are useful in diagnosing or monitoring
 XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 XX CC islet, lung, bone marrow or stem cell transplant rejection,
 XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
 XX CC individual. The method is also useful in assessing the immune status of
 XX CC an individual. The methods are also useful in diagnosing and monitoring
 XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 XX CC viral, bacterial or fungal infection. The present sequence represents a
 XX CC protein that is encoded by the mRNA of the invention.
 XX SQ Sequence 362 AA;
 Query Match 100.0%; Score 274; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 9.4e-250;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSRGRGEPRIAYEVYDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 60
 DB 22 GSHSLRYFSTAVSRGRGEPRIAYEVYDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 81
 QY 61 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQNGGDMGPDGRLRLRGYHQAYDG 120
 DB 82 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQNGGDMGPDGRLRLRGYHQAYDG 141
 QY 121 KYIISLNEDLRSWTADTVAQIQTFYAEYAEFRYILEGECLELLRRLYENGKETLQ 180
 DB 142 KYIISLNEDLRSWTADTVAQIQTFYAEYAEFRYILEGECLELLRRLYENGKETLQ 201
 QY 181 RADPPKARVAHPISDHEATRLCWAALGFYPAEITLTWQDGEETQDTLVEFRPAGDGT 240
 DB 202 RADPPKARVAHPISDHEATRLCWAALGFYPAEITLTWQDGEETQDTLVEFRPAGDGT 261
 QY 241 FQKWAAVVPSGEGRYTCHVQHEGLFQPLILRW 274

DB 262 FQKWAAVVPSGEGRYTCHVQHEGLFQPLILRW 295
 RESULT 8
 ADJ70081
 ID ADJ70081 standard; protein; 442 AA.
 XX AC ADJ70081;
 XX DT 06-MAY-2004 (first entry)
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID1897.
 XX KW mitochondrial; human; screening assay; diabetes mellitus;
 XX KW Huntington's disease; osteoarthritis; LHON;
 XX KW Leber's hereditary optic neuropathy; LHON;
 XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 XX KW osteopathic; ophthalmological; cytostatic.
 XX OS Homo sapiens.
 XX PN WO2003087768-A2.
 XX PD 23-OCT-2003.
 XX PF 04-APR-2003; 2003WO-US010870.
 XX PR 12-APR-2002; 2002US-0372843P.
 XX PR 17-JUN-2002; 2002US-038987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX PA (MITO-) MITOKOR.
 XX PA (BUCK-) BUCK INST AGE RES.
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX PI Warnock DE;
 XX DR WPI; 2003-845369/78.
 XX PT Identifying a mitochondrial target for drug screening assays and for
 XX PT treating diseases associated with altered mitochondrial function,
 XX PT comprises detecting a modified polypeptide in a sample and correlating
 XX PT with the disease.
 XX PS Claim 1; SEQ ID NO 1887; 180pp; English.
 XX CC This invention relates to novel mitochondrial targets that can be used
 XX CC for therapeutic intervention in treating a disease associated with
 XX CC altered mitochondrial function. Specifically, it refers to a method for
 XX CC identifying proteins of the human heart mitochondrial proteome that are
 XX CC useful for drug screening assays, as well as therapeutic targets. The
 XX CC present invention describes a method for identifying such proteins that
 XX CC can be used in the treatment of various diseases associated with altered
 XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
 XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 XX CC compositions have neuroprotective, nontropic, antidiabetic,
 XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 XX CC cytostatic activities. This polypeptide sequence is a human heart
 XX CC mitochondrial protein of the invention.
 XX SQ Sequence 442 AA;
 Query Match 100.0%; Score 274; DB 7; Length 442;
 Best Local Similarity 100.0%; Pred. No. 1.1e-249;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSRGRGEPRIAYEVYDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 60
 DB 22 GSHSLRYFSTAVSRGRGEPRIAYEVYDDTQFLRFDSDAAIPRMEPRPFWQEGPQYW 81

QY 61 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMPDGLRLRGYHQHAYDG 120
 DB 82 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMPDGLRLRGYHQHAYDG 141
 QY 121 KQYISLNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELLRLRYLNGKETLQ 180
 DB 142 KQYISLNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELLRLRYLNGKETLQ 201
 QY 181 RADPPKARVAHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTVELVETRPAGDGT 240
 DB 202 RADPPKARVAHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTVELVETRPAGDGT 261
 QY 241 FQKWAADVVP 250
 DB 262 FQKWAADVVP 580

RESULT 9
 ID ABG26726 standard; protein; 677 AA.
 AC ABG26726;
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #26717.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS90913.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 57085; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application of mutations
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 677 AA;
 QY Query Match 91.2%; Score 250; DB 4; Length 677;
 DB Best Local Similarity 100.0%; Pred. No. 6.6e-227;
 QY Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 GSHSLRYFTSTAVSRGRCGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 60
 QY 331 GSHSLRYFTSTAVSRGRCGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRFVWQEGPQYW 390
 QY 61 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMPDGLRLRGYHQHAYDG 120
 DB 391 EWTGAKANAQTDVALNLLRRYNSAGSHLQMGCDMPDGLRLRGYHQHAYDG 450
 QY 121 KQYISLNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELLRLRYLNGKETLQ 180
 DB 451 KQYISLNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELLRLRYLNGKETLQ 510
 QY 181 RADPPKARVAHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTVELVETRPAGDGT 240
 DB 511 RADPPKARVAHHPISDHEATLRCWALGFYPAEITLTWQDGEEOQDTVELVETRPAGDGT 570
 QY 241 FQKWAADVVP 250
 DB 571 FQKWAADVVP 580
 RESULT 10
 ID AAB43986 standard; protein; 271 AA.
 XX AAB43986;
 DT 08-FEB-2001 (first entry)
 DE Human cancer associated protein sequence SEQ ID NO:1431.
 XX Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
 KW antidiabetic; antiaesthetic; antirheumatic; antithyroid; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.
 XX Homo sapiens.
 OS WO200055350-A1.
 PN 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US005882.
 XX 12-MAR-1999; 99US-0124270P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI; 2000-587533/55.
 DR N-PSDB; AAC78195.
 XX Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer.
 XX

PS Claim 11; Page 2115-2116; 2352pp; English.
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; tumorigenic; immunomodulatory;
 CC antidiabetic; antiaesthetic; antirheumatic; antithrombotic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
 CC neotropic; vasotropic; antipsoriatic and angiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilization of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention
 CC
 SQ Sequence 271 AA;

Query Match 88.0%; Score 241; DB 3; Length 271;
 Best Local Similarity 100.0%; Pred. No. 9.8e-219;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYSTAVSRGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 60
 DB 28 GSHSLRYSTAVSRGCEPRYIAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 87
 QY 61 EWTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMPDGLLRGVHAYDYG 120
 DB 88 EWTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMPDGLLRGVHAYDYG 147
 QY 121 KYIISLNEQLRSWTAADTVAQITQRYEABEYAEFRYLEGECLELLRRYLENGKETLQ 180
 DB 148 KYIISLNEQLRSWTAADTVAQITQRYEABEYAEFRYLEGECLELLRRYLENGKETLQ 207
 QY 181 RADPPKAVHAPHISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVEPTRAGDT 240
 DB 208 RADPPKAVHAPHISDHEATLRCWALGFYPAEITLTWQDGEEOQTDELVEPTRAGDT 267
 QY 241 F 241
 DB 268 F 268

RESULT 11
 AAG64619 standard; protein; 215 AA.
 AC AAG64619;
 XX
 XX 12-SEP-2001 (first entry)
 XX Human cancer cell specific HLA-F antigen SEQ ID 6.
 XX
 XX HLA-F antigen; cancer cell specific; human.
 XX Homo sapiens.
 XX JP2001095584-A.
 XX
 XX 10-APR-2001.
 XX
 XX 30-SEP-1999; 99JP-00279566.
 XX
 XX 30-SEP-1999; 99JP-00279566.
 XX

PA (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 XX (KIMU/) KIMURA K.
 DR WPI: 2001-360493/38.
 DR N-PSDB; AAB45557.
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX Claim 1; Page 11-12; 12pp; Japanese.
 XX This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer, in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
 CC sequence represents the cancer cell-specific HLA-F antigen of the
 CC invention
 XX
 SQ Sequence 215 AA;

Query Match 78.5%; Score 215; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.7e-194;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWTTGYAKANAQTDVALNLL 82
 DB 1 IAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYWTTGYAKANAQTDVALNLL 60
 QY 83 PRYNQSEAGSHTLQGMNGCDMPDGLLRGVHAYDYGKDYISLNEQLRSWTAADTVAQI 142
 DB 61 PRYNQSEAGSHTLQGMNGCDMPDGLLRGVHAYDYGKDYISLNEQLRSWTAADTVAQI 120
 QY 143 TORFYAEABEYAEFRYLEGECLELLRRYLENGKETLQADPPKAVHAPHISDHEATLR 202
 DB 121 TORFYAEABEYAEFRYLEGECLELLRRYLENGKETLQADPPKAVHAPHISDHEATLR 180
 QY 203 CWNLCGFYPAEITLTWQDGEEOQTDELVEPTRAG 237
 DB 181 CWNLCGFYPAEITLTWQDGEEOQTDELVEPTRAG 215

RESULT 12
 ADF55589
 ID ADF55589 standard; protein; 215 AA.
 XX ADF55589;
 XX
 XX 12-FEB-2004 (first entry)
 XX
 XX Fragment #2 of human cancer-cell specific HLA-F antigen.
 XX Cancer; human leukocyte antigen-F; HLA-F;
 XX cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 XX major histocompatibility complex; MHC; cancer cell; human.
 XX Homo sapiens.
 XX JP2003012544-A.
 XX
 XX 15-JAN-2003.
 XX
 XX 27-MAR-2002; 2002JP-00088991.
 XX
 XX 27-MAR-2001; 2001JP-00090121.
 XX (EGAW/) EGAWA K.
 XX (MEDI-) MEDINET KK.
 XX (KIMU/) KIMURA Y.
 XX
 XX WPI: 2003-486263/46.
 XX N-PSDB; ADF55586.
 XX

PT Agent for preventing and treating cancer, comprising human leukocyte
 XX antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 PS Claim 7; SEQ ID NO 6; 19pp; Japanese.
 XX
 CC The present invention relates to an agent for preventing or treating
 CC cancer. The agent comprises a portion or a complete sequence of a human
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is
 CC unrestricted to the major histocompatibility complex (MHC) and specific
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
 CC is useful for treating or preventing cancer. A cell capable of presenting
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
 CC for diagnosing cancer. The present sequence represents part of the human
 CC cancer-cell specific HLA-F antigen.
 XX
 SQ Sequence 215 AA;

Query Match 78.5%; Score 215; DB 7; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.7e-194;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 IAVEVDDTQFLRPSDAATPRMEPREPVEQPGQYWEWTTGYAKANAQTDRAVLRNL 82
 DB 1 IAVEVDDTQFLRPSDAATPRMEPREPVEQPGQYWEWTTGYAKANAQTDRAVLRNL 60
 QY 83 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHGHAYDGRDYISLNEDLSRMTAADTVAQI 142
 DB 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHGHAYDGRDYISLNEDLSRMTAADTVAQI 120
 QY 143 TORFEAEVABEAFRTYLEGCELELRVLENGKETLORADPPKARVAHPISDHEATLR 202
 DB 121 TORFEAEVABEAFRTYLEGCELELRVLENGKETLORADPPKARVAHPISDHEATLR 180
 QY 203 CWALGFYPABITLTWRDGEQTDTELVTETPAG 237
 DB 181 CWALGFYPABITLTWRDGEQTDTELVTETPAG 215

RESULT 13
 AAG00209
 ID AAG00209 standard; protein; 120 AA.
 XX AC AAG00209;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 4290.
 XX KW Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EPI033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GIST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX DR N-PSDB; AAC00215.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 120 AA;

Query Match 36.1%; Score 99; DB 3; Length 120;
 Best Local Similarity 100.0%; Pred. No. 4.3e-85;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSRGCRGEPRIAYVYDDTQFLRPSDAATPRMEPREPVEQPGQY 60
 DB 22 GSHSLRYFSTAVSRGCRGEPRIAYVYDDTQFLRPSDAATPRMEPREPVEQPGQY 81
 QY 61 EMTTGVAKANAQTDRAVLRNLRRYNQSEAGSHTLQGMN 99
 DB 82 EMTTGVAKANAQTDRAVLRNLRRYNQSEAGSHTLQGMN 120

RESULT 14
 ABP42931
 ID ABP42931 standard; protein; 186 AA.
 XX AC ABP42931;
 XX DT 22-AUG-2002 (first entry)
 XX DE Human ovarian antigen HPRD737, SEQ ID NO:4063.
 XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX OS Homo sapiens.
 XX PN WO200200677-A1.
 XX PD 03-JAN-2002.
 XX PF 07-JUN-2001; 2001WO-US018569.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 XX DR N-PSDB; ABQ56008.
 XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian

PT cancer), immune disorders, cardiovascular disorders and neurological
 XX diseases.

PS Claim 11; SEQ ID NO 4063; 2922pp; English.

XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 186 AA;

Query Match 25.5%; Score 70; DB 5; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.3e-57;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YAKANAQTDVVALNRLRRYNSAGSHTLQGMNGCDMGDPDGRLLRGYHQHAYDGKDYIS 125
 Db 1 YAKANAQTDVVALNRLRRYNSAGSHTLQGMNGCDMGDPDGRLLRGYHQHAYDGKDYIS 60

QY 126 LNEDLRSWTA 135

Db 61 LNEDLRSWTA 70

RESULT 15

ID AB057084

XX AB057084 standard; protein; 96 AA.

AC AB057084;

XX 29-JUL-2004 (first entry)

DE Human genome derived single exon protein #3318.

XX Human; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX Homo sapiens.

OS US2003194704-A1.

PN 16-OCT-2003.

PD 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX

PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.

XX Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 45; SEQ ID NO 30718; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 96 AA;

Query Match 24.8%; Score 68; DB 8; Length 96;

Best Local Similarity 100.0%; Pred. No. 6.1e-56;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 DPPKARVAHHPISDHEATLRCWALGFYPAITITWTQRDGEQQTDELVETRPAGDGTQ 242

Db 2 DPPKARVAHHPISDHEATLRCWALGFYPAITITWTQRDGEQQTDELVETRPAGDGTQ 61

QY 243 KWAAYVVP 250

Db 62 KWAAYVVP 69

Search completed: December 15, 2004, 18:20:02

Job time : 125.151 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:24:34 ; Search time 111.505 Seconds
(without alignments)
877.689 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRPFSTAVSRGRGP.....QRYTCHVQHGELPQLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1585576 seqs, 357178320 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	274	100.0	274	11	US-09-819-371-5
2	274	100.0	362	14	US-10-257-021-82
3	274	100.0	442	16	US-10-408-765A-1887
4	241	88.0	271	9	US-09-925-301-1431
5	175	63.9	362	11	US-09-819-371-4
6	119	43.4	215	11	US-09-819-371-6
7	70	25.5	186	15	US-10-264-049-4063
8	68	24.8	96	14	US-10-029-386-30718
9	44	16.1	77	14	US-10-029-386-34273
10	44	16.1	91	14	US-10-029-386-31089
11	44	16.1	104	9	US-09-925-302-835
12	44	16.1	104	10	US-09-925-302-835
13	43	15.7	476	17	US-10-430-984-16

14	43	15.7	500	17	US-10-430-984-15	Sequence 15, Appl
15	40	14.6	78	14	US-10-029-386-30752	Sequence 30752, A
16	40	14.6	371	15	US-10-085-198-72	Sequence 72, Appl
17	40	14.6	371	15	US-10-210-172-156	Sequence 156, App
18	39	14.2	91	9	US-09-864-761-38005	Sequence 38005, A
19	39	14.2	92	15	US-10-380-880-5	Sequence 5, Appl
20	39	14.2	169	16	US-10-741-601-383	Sequence 383, App
21	39	14.2	198	16	US-10-741-601-387	Sequence 387, App
22	39	14.2	234	15	US-10-380-880-8	Sequence 8, Appl
23	39	14.2	251	16	US-10-741-601-384	Sequence 384, App
24	39	14.2	284	14	US-10-104-047-3648	Sequence 3648, App
25	39	14.2	326	15	US-10-380-880-7	Sequence 7, Appl
26	39	14.2	338	16	US-10-741-601-380	Sequence 380, App
27	39	14.2	338	16	US-10-741-601-388	Sequence 388, App
28	39	14.2	343	16	US-10-741-601-379	Sequence 379, App
29	39	14.2	379	14	US-10-093-463-78	Sequence 78, Appl
30	39	14.2	379	15	US-10-210-172-160	Sequence 160, App
31	38	13.9	145	9	US-09-810-560-8	Sequence 8, Appl
32	36	13.1	45	14	US-10-029-386-28883	Sequence 28883, A
33	32	11.7	91	9	US-09-864-761-35461	Sequence 35461, A
34	32	11.7	110	9	US-09-796-692-799	Sequence 799, App
35	32	11.7	110	9	US-09-796-692-2139	Sequence 2139, App
36	32	11.7	110	14	US-10-040-862-799	Sequence 799, App
37	32	11.7	110	14	US-10-040-862-2139	Sequence 2139, App
38	32	11.7	110	15	US-10-057-475B-799	Sequence 799, App
39	32	11.7	110	15	US-10-057-475B-2139	Sequence 2139, App
40	32	11.7	110	15	US-10-154-884B-799	Sequence 799, App
41	32	11.7	110	15	US-10-154-884B-2139	Sequence 2139, App
42	32	11.7	110	16	US-10-764-324-799	Sequence 799, App
43	32	11.7	110	16	US-10-764-324-2139	Sequence 2139, App
44	32	11.7	196	15	US-10-262-839-48	Sequence 48, Appl
45	32	11.7	198	15	US-10-264-049-3505	Sequence 3505, App

ALIGNMENTS

RESULT 1

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match	100.0%;	Score 274;	DB 11;	Length 274;
Best Local Similarity	100.0%;	Pred. No. 2.6e-260;		
Matches 274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GSHSLRPFSTAVSRGRGPRIAYEVDTQFLRFDSDAAIPRMPRPFWVEQGPQYW	60	
Db	1	GSHSLRPFSTAVSRGRGPRIAYEVDTQFLRFDSDAAIPRMPRPFWVEQGPQYW	60	
QY	61	EWTTGYAKAQTDRVALRNLRLRYNQSAGSHTLQMGNCMDGPDGRLLRGVHQHAYDG	120	
Db	61	EWTTGYAKAQTDRVALRNLRLRYNQSAGSHTLQMGNCMDGPDGRLLRGVHQHAYDG	120	
QY	121	KDYISLNEDELSWTAADTAQITQRFYEABEYAEFRTYLEGECLELLRLRYLNGKETIQ	180	
Db	121	KDYISLNEDELSWTAADTAQITQRFYEABEYAEFRTYLEGECLELLRLRYLNGKETIQ	180	
QY	181	RADPFKAHVHPISDHEATLRWCWALGFYPAEITLTWQRDGBEQTQDTLVEFRPADGT	240	

Db 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEVTRPAGDGT 240
 Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274
 Db 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274

RESULT 2
 US-10-257-021-82
 ; Sequence 82, Application US/10257021
 ; Publication No. US20030211498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morin, Patrice J.
 ; APPLICANT: Sherman-Baut, Cheryl A.
 ; APPLICANT: Pizer, Ellen S.
 ; APPLICANT: Hough, Colleen D.
 ; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
 ; FILE REFERENCE: 14014.0369U2
 ; CURRENT APPLICATION NUMBER: US/10/257,021
 ; PRIOR FILING DATE: 2002-10-03
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/194,336
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 82
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-257-021-82

Query Match 100.0%; Score 274; DB 14; Length 362;
 Best Local Similarity 100.0%; Pred. No. 3.3e-260;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 60
 Db 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 81
 Qy 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120
 Db 82 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 141
 Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180
 Db 142 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 201
 Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEVTRPAGDGT 240
 Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEVTRPAGDGT 261
 Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274
 Db 262 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 295

RESULT 3
 US-10-408-765A-1887
 ; Sequence 1887, Application US/10408765A
 ; Publication No. US2004010187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1887
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1887

Query Match 100.0%; Score 274; DB 16; Length 442;
 Best Local Similarity 100.0%; Pred. No. 3.9e-260;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 60
 Db 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 81
 Qy 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120
 Db 82 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 141
 Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180
 Db 142 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 201
 Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEVTRPAGDGT 240
 Db 202 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQTDTELVEVTRPAGDGT 261
 Qy 241 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 274
 Db 262 FQKAAVVPVSGEQRVTCHVQHEGLPQPLILRW 295

RESULT 4
 US-09-925-301-1431
 ; Sequence 1431, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 1431
 ; LENGTH: 271
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-301-1431

Query Match 88.0%; Score 241; DB 9; Length 271;
 Best Local Similarity 100.0%; Pred. No. 6.3e-228;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 60
 Db 28 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQYW 87
 Qy 61 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 120
 Db 88 EWTGAKANAQTDRAVRLNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGYHCHAYDG 147
 Qy 121 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 180
 Db 148 KDYSISNEDLSRWTAAADTVAQITQRFYEAEEYAEFFTYLEGECELELLRRLRYLENGKETLQ 207

QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLWETRPAGDGT 240
DB 208 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLWETRPAGDGT 267
QY 241 F 241
DB 268 F 268

RESULT 5

US-09-819-371-4
; Sequence 4, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

Query Match 53.9%; Score 175; DB 11; Length 362;

Best Local Similarity 100.0%; Pred. No. 5.1e-163;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMPRPFWVEQGPQYW 60
DB 22 GSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSDAAIPRMPRPFWVEQGPQYW 81
QY 61 EWTTGYAKANAQTRVALNRLRLRYNQSEAGSHLTQMGNCMDGPGDRLLRGHQYAYDG 120
DB 82 EWTTGYAKANAQTRVALNRLRLRYNQSEAGSHLTQMGNCMDGPGDRLLRGHQYAYDG 141
QY 121 KDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRRLYLENG 175
DB 142 KDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFTYLGECLLELLRRLYLENG 196

RESULT 6

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 43.4%; Score 119; DB 11; Length 215;

Best Local Similarity 100.0%; Pred. No. 3e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 DKQYISLNEDLSRWTADTVAQITQRFYEAEYAEFFTYLGECLLELLRRLYLENGKET 178
DB 97 DKQYISLNEDLSRWTADTVAQITQRFYEAEYAEFFTYLGECLLELLRRLYLENGKET 156
QY 179 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLWETRPAG 237

DB 157 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQDGBEQTQDTLWETRPAG 215

RESULT 7

US-10-264-049-4063
; Sequence 4063, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Bitsee et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4063
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (176)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:

; NAME/KEY: MISC FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4063

Query Match 25.5%; Score 70; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.4e-60;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 YAKNAGTDAVALNLLRRNQSEAGSHLQNGMGCDGPDGRLLRGVHGHAYDKDYIS 125

Db 1 YAKNAGTDAVALNLLRRNQSEAGSHLQNGMGCDGPDGRLLRGVHGHAYDKDYIS 60

Qy 126 LNEEDLSWTA 135

Db 61 LNEEDLSWTA 70

RESULT 8

US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

Query Match 24.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 DPKAHVAHPIISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETRPAGDGTFO 242

Db 2 DPKAHVAHPIISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETRPAGDGTFO 61

Qy 243 KWAAVVVP 250

Db 62 KWAAVVVP 69

RESULT 9

US-10-029-386-34273
; Sequence 34273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34273

; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273

Query Match 16.1%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 267

Db 25 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 68

RESULT 10

US-10-029-386-31089
; Sequence 31089, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31089
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004204.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52
US-10-029-386-31089

Query Match 16.1%; Score 44; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 5.9e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 267

Db 41 QTQDTLVTETRPAGDGTFOKWAAVVVPSEGEQRYTCHVQHEGLP 84

RESULT 11

US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 835

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/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (95)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match
Best Local Similarity 16.1%; Score 44; DB 9; Length 104;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 267
Db 32 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 75

RESULT 12
US-09-925-302-835
/ Sequence 835, Application US/09925302
/ Publication No. US20030064072A9
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 835
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (95)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match
Best Local Similarity 16.1%; Score 44; DB 10; Length 104;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 267
Db 32 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 75

RESULT 13
US-10-430-984-16
/ Sequence 16, Application US/10430984
/ Publication No. US20040225112A1
/ GENERAL INFORMATION:
/ APPLICANT: The Board of Trustees of the University of Arkansas
/ APPLICANT: Crew, Mark D
/ TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
/ FILE REFERENCE: 8793-53098
/ CURRENT APPLICATION NUMBER: US/10/430,984
/ CURRENT FILING DATE: 2003-05-09
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 16
/ LENGTH: 476
/ TYPE: PRT
/ ORGANISM: human leukocyte antigen E-Single chain dimer
US-10-430-984-16
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Query Match
Best Local Similarity 15.7%; Score 43; DB 17; Length 476;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 267
Db 364 TQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 406

RESULT 14
US-10-430-984-15
/ Sequence 15, Application US/10430984
/ Publication No. US20040225112A1
/ GENERAL INFORMATION:
/ APPLICANT: The Board of Trustees of the University of Arkansas
/ APPLICANT: Crew, Mark D
/ TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
/ FILE REFERENCE: 8793-53098
/ CURRENT APPLICATION NUMBER: US/10/430,984
/ CURRENT FILING DATE: 2003-05-09
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 15
/ LENGTH: 500
/ TYPE: PRT
/ ORGANISM: human leukocyte antigen E-Single chain Trimer
US-10-430-984-15

Query Match
Best Local Similarity 15.7%; Score 43; DB 17; Length 500;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 267
Db 388 TQDTLVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 430

RESULT 15
US-10-029-386-30752
/ Sequence 30752, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
/ FILE REFERENCE: ABOICA-X-2
/ CURRENT APPLICATION NUMBER: US/10/029,386
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 34288
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 30752
/ LENGTH: 78
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR6.1
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 48
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 57
/ OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUATE 7.00e-24
US-10-029-386-30752

Query Match
Best Local Similarity 14.6%; Score 40; DB 14; Length 78;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 TELVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 267
Db 29 TELVETRPAGDGTQKWAADVVPSSGEQRVTCHVQHEGLP 68
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Fri Dec 17 09:27:20 2004

us-09-819-371-5.Oligo.rapb

Page 6

Search completed: December 15, 2004, 18:41:48
Job time : 112.505 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:30 ; Search time 111.677 Seconds
(without alignments)
1107.709 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 215
Sequence: 1 TAVEYVDQTFLRFDSDAAI.....QRDGEQTQDTLVEVETRPAG 215

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	119	55.3	324	2	Q861F0
3	119	55.3	346	2	Q8MGO1
4	119	55.3	346	2	Q85IT2
5	119	55.3	346	2	Q8WLP5
6	119	55.3	346	2	Q8DU20
7	119	55.3	346	2	Q8DU28
8	119	55.3	346	2	AAH62991
9	119	55.3	362	1	HLAF HUMAN
10	119	55.3	362	2	Q7YR27
11	119	55.3	362	2	BAC54915
12	119	55.3	460	2	Q85HCO
13	95	44.2	254	2	Q860R0
14	71	33.0	349	2	Q8ZUW0
15	71	33.0	349	2	BAC86108
16	70	32.6	346	1	IC28_PANTR
17	59	27.4	59	2	Q8T094
18	54	25.1	91	2	Q8TPX7
19	53	24.7	355	2	Q767W6
20	53	24.7	355	2	BAD18942
21	47	21.9	314	2	Q860F6
22	47	21.9	348	1	HLAF_MACMU
23	45	20.9	330	2	Q30713
24	45	20.9	359	2	Q30711
25	43	20.0	316	2	Q29958
26	43	20.0	351	2	Q70PL7
27	43	20.0	351	2	Q70PM0
28	43	20.0	351	2	CAD89636
29	43	20.0	351	2	CAD89639
30	43	20.0	353	2	Q9MXS6
31	43	20.0	353	2	Q9MXS7

32	43	20.0	354	2	Q703T0
33	43	20.0	354	2	Q70UE5
34	43	20.0	354	2	Q70UE6
35	43	20.0	354	2	Q70UE7
36	43	20.0	354	2	CAD85765
37	43	20.0	354	2	CAD85765
38	43	20.0	354	2	CAD85767
39	43	20.0	354	2	CAD83073
40	43	20.0	365	2	Q617A3
41	43	20.0	365	2	Q9MXS5
42	41	19.1	330	2	Q860E9
43	41	19.1	333	2	Q860E7
44	41	19.1	337	2	Q70PK6
45	41	19.1	337	2	CAD89650

ALIGNMENTS

RESULT 1					
Q861E9	ID	Q861E9	PRELIMINARY;	PRT;	324 AA.
AC	Q861E9;				
DT	01-JUN-2003	(Tremblrel. 24, Created)			
DT	01-JUN-2003	(Tremblrel. 24, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	MHC class I antigen (Fragment).				
GN	Name=HLA-F;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Liu Y., Xu L., Zeng Y., He X.;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY221102; AAC34407.1;				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0006955; P:immune response; IEA.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig.c1.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR001039; MHC I.				
DR	Pfam; PF07654; C1-set; 1.				
DR	Pfam; PF00129; MHC I; 1.				
DR	PRINTS; PR01638; MHCCLASSI.				
DR	PRODOM; PD000050; MHC.I; 1.				
DR	PROSITE; PS00835; IG_LIKE; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
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FT	NON_TER 324				
SQ	SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;				
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Best Local Similarity 100.0%; Pred.No.5.9e-117;					
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	97	DKGDIYISLNDLRSWTAADTVAQITQFYAEAYAEFEFTYLEGECLELLRYLENGKET 156			
Db	136	DKGDIYISLNDLRSWTAADTVAQITQFYAEAYAEFEFTYLEGECLELLRYLENGKET 195			
Qy	157	LQRADPPKAVHHPHPSDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVETRPAG 215			
Db	196	LQRADPPKAVHHPHPSDHEATLRCWALGFYPAEITLTWQDGEQOTQDTLVEVETRPAG 254			
RESULT 2					
Q861F0	ID	Q861F0	PRELIMINARY;	PRT;	324 AA.
AC	Q861F0;				
DT	01-JUN-2003	(Tremblrel. 24, Created)			
DT	01-JUN-2003	(Tremblrel. 24, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			

DE	Nonclassical MHC class I antigen (Fragment).
OS	Name=HLA-F;
GN	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_taxID=9606;
OC	[1]_
OC	SEQUENCE FROM N.A.
RRP	He X., Xu L., Liu Y., Zeng Y.;
RRP	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RRL	EMBL; AY216682; AAC037689.1; -
DR	HSSP; Q29961; 1HSA.
DR	GO; GO:0016020; P:immune response; IEA.
DR	GO; GO:0006955; C:membrane; IEA.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001039; MHC_I.
DR	Pfam; PF07654; Cl-set; 1.
DR	Pfam; PF00123; MHC_I; 1.
DR	PRINTS; PR01638; MHCCLASSI.
DR	ProDom; PD000050; MHC_I; 1.
DR	SMART; SM00407; Igcl; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
FT	NON_TER 1
FT	NON_TER 324 324
SSQ	SEQUENCE 324 AA; 36518 MW; E3E02817D2716F4 CRC64;
Query Match 55.3%; Score 119; DB 2; Length 324;	
Best Local Similarity 100.0%; Pred. No. 5.9e-117;	
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	97 DKDYISINEDLSWTAADTVAGIOTRFYEAEYAEAEPTYLEGECLELLRYLENGKET 156
Ddb	136 DKGDYISINEDLSWTAADTVAGIOTRFYEAEYAEAEPTYLEGECLELLRYLENGKET 195
Qy	157 LQADPPKAVHHPISDHEATLRWCALGFYPAEITLTWQDGEQTQDTLVETRPAG 215
Ddb	196 LQADPPKAVHHPISDHEATLRWCALGFYPAEITLTWQDGEQTQDTLVETRPAG 254
RESULT 3	
Q8MGQ1 PRELIMINARY; PRT; 346 AA.	
ID	Q8MGQ1
AC	Q8MGQ1;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	MHC class Ib antigen.
GN	Name=HLA-F;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_taxID=9606;
OC	[1]_
OC	SEQUENCE FROM N.A.
RRP	Ishtitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RRP	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RRP	SEQUENCE FROM N.A.
RRP	Pyo C.-W., Ishtitani A., Moore Y.F., Geraghty D.E.;
RRP	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RRL	EMBL; AF523284; AAM74979.1; -
DR	EMBL; AF523291; AAM74986.1; -
DR	EMBL; AF523232; AAM74987.1; -
DR	EMBL; AF523232; AAM74987.1; -
DR	EMBL; AY645748; AAT73231.1; -
DR	EMBL; AY645754; AAT73237.1; -
DR	HSSP; Q29961; 1HSA.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.


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Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199
QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215
Db 200 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

RESULT 7
Q6DU28
ID Q6DU28 PRELIMINARY; PRT; 346 AA.
AC Q6DU28;
DT 01-OCT-2004 (TRENBLrel. 28, Created)
DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE 01-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE MHC class II antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY645747; AAT73230.1; -.
SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;

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Query Match 55.3%; Score 119; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.3e-117;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199

QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215
Db 200 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

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RESULT 8
AAH62991
ID AAH62991 PRELIMINARY; PRT; 346 AA.
AC AAH62991;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DE HLA-F protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22389257; Pubmed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP
SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062991; AAH62991.1; -.
SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.3e-117;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRWSAATVAQITQRFYEAEEYAEFFRYLEGECELELLRRYLENGKET 199

QY 157 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 215
Db 200 LORADPPKAAVHAHPISDHEATLRCWALGFYPAEITLTWQDGEOTQDTLVEVTRPAG 258

RESULT 9
HLAF HUMAN
ID HLAF HUMAN STANDARD; PRT; 362 AA.
AC P3051l; Q9TP68;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F
DE antigen) (Leukocyte antigen F) (CDA12).
GN Name=HLA-F; Synonyms=HLAF, HLA-5.4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
SEQUENCE FROM N.A.
RX MEDLINE=90111605; Pubmed=1688605;
RA Geraghty D.E., Wei X., Orr H.T., Koller B.H.;
RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of
RT a class I coding sequence linked to a novel transcribed repetitive
RT element.";
RL J. Exp. Med. 171:1-18 (1990).
RN [2]
RP
SEQUENCE FROM N.A.
RX MEDLINE=91197889; Pubmed=1707659;
RA Lury D., Epstein H., Holmes N.;
RT "The human class I MHC gene HLA-F is expressed in lymphocytes.";
RL Int. Immunol. 2:531-537 (1990).
RN [3]
RP
SEQUENCE FROM N.A.
RX MEDLINE=20189617; Pubmed=10727083;
RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcellet M.,
RA Mottier S., Dreano S., Gattus M.T., Hitte C., Soriano N., Galibert F.;
RT "A 356-Kb sequence of the subtelomeric part of the MHC class I
RT region.";
RL DNA Seq. 10:263-299 (1999).
RN [4]
RP
SEQUENCE FROM N.A.
RX MEDLINE=2293763; Pubmed=14574404; DOI=10.1038/nature02055;
RA Shihina S., Tamiya G., Oka A., Inoko H.;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

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RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.F.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark S.Y., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Finlay L.M., Gilson C.J., Garner P., Garnett J., Ghori M.J.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.J., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamratt D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McIlroy K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.M.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H. Wild A., Willey D.J., Wilmer T.B., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulterson J.E., Dunham I., Rogers J., Beck S.;
RA "The DNA sequence and analysis of human chromosome 6.";
RL Nature 425:805-811(2003).
CC -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC immune system.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC microglobulin).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; X17093; CAA34947.1; -;
CC EMBL; AF055066; AAC24827.1; -;
CC EMBL; AF000521; BAB63337.1; -;
CC EMBL; AL022723; CAB46623.1; -;
CC PIR; A60384; A60384.
CC HSSP; Q29961; LHSA.
CC Genew; HGNC:4963; HLA-F.
CC MIM; 143110; -;
CC GO; GO:0030106; F:MHC class I receptor activity; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001039; MHC_I.
CC InterPro; IPR010579; MHC_I_C.
CC Pfam; PF00047; ig_1.
CC Pfam; PF00129; MHC_I_1.
CC Pfam; PF06623; MHC_I_C_1.
CC PRINTS; PF06623; MHC_I_C_1.
CC PRINTS; PF01638; MHCCLASSI.
CC ProDom; PD000050; MHC_I_1.
CC SMART; SM00407; IGc1; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC Glycoprotein; MHC I; Polymorphism; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 362 HLA class I histocompatibility antigen,
FT alpha chain F.
FT DOMAIN 22 111 Extracellular alpha-1.
FT DOMAIN 112 203 Extracellular alpha-2.
FT DOMAIN 204 295 Extracellular alpha-3.

FT DOMAIN 296 305 Connecting peptide.
FT TRANSMEM 306 329
FT DOMAIN 330 362 Cytoplasmic tail.
FT DISULFID 122 185 By similarity.
FT DISULFID 224 280 By similarity.
FT CARBOHYD 107 107 N-linked (GLCNAC...) (By similarity).
FT VARIANT 272 S -> P (in dbSNP:1736924).
FT /FTID=VAR_018327.
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;
Query Match 55.3%; Score 119; DB 1; Length 362;
Best Local Similarity 100.0%; Pred.No. 6.5e-117; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;
QY 97 DGKDYISLNLRSWTAADTVAQITQRFYAEAEFEFTYLEGECELLRRYLENGKET 156
DB 140 DGKDYISLNLRSWTAADTVAQITQRFYAEAEFEFTYLEGECELLRRYLENGKET 199
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFPYAEITLTWQDGEQTDTELVEHPAG 215
DB 200 LQADPPKAAVHHPISDHEATLRCWALGFPYAEITLTWQDGEQTDTELVEHPAG 258
RESULT 10
QYR27 PRELIMINARY; PRT; 362 AA.
AC QYR27
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Class Ib.
GN Name=Patr-P;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
CX NCBI_TaxId=9998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463;
RA Anzai T., Shina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Katsuki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwanoto C., Uehara Y., Imanishi T.,
RA Meyer A., Ikoe K., Gojobori T., Bahram S., Inoko H.;
RA "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
RL EMBL; AB100087; BAC78191.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR InterPro; IPR010579; MHC_I_C.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00129; MHC_I_1.
DR Pfam; PF06623; MHC_I_C_1.
DR ProDom; PD000050; MHC_I_1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;
Query Match 55.3%; Score 119; DB 2; Length 362;
Best Local Similarity 100.0%; Pred.No. 6.5e-117; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;
QY 97 DGKDYISLNLRSWTAADTVAQITQRFYAEAEFEFTYLEGECELLRRYLENGKET 156
DB 140 DGKDYISLNLRSWTAADTVAQITQRFYAEAEFEFTYLEGECELLRRYLENGKET 199

QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 258

RESULT 11
 BACS4915
 ID BACS4915 PRELIMINARY; PRT; 362 AA.
 AC BACS4915;
 DT 02-MAR-2004 (TREMELrel. 27, Created)
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
 DE 02-MAR-2004 (TREMELrel. 27, Last annotation update)
 DE Major histocompatibility complex, class I, F.
 GN HLA-F.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shina T., Oka M., Katsuyama Y., Hashimoto N., Inoko H.;
 RT "Genome diversity in HLA: A new strategy for detection of genetic
 RT polymorphisms in expressed genes within the HLA class III and class I
 RT regions."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB088082; BACS4915.1;
 SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 55.3%; Score 119; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 6.5e-117; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQFYAEAEYAEAEFTYLEGCELELLRRYLENGKET 156
 DB 140 DGKDYISLNEDLSRWSAATVAQITQFYAEAEYAEAEFTYLEGCELELLRRYLENGKET 199

QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 258

RESULT 12
 Q95HCO
 ID Q95HCO PRELIMINARY; PRT; 460 AA.
 AC Q95HCO;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE HLA-F protein (Fragment).
 GN Name=HLA-F;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.;
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009260; AAH09260.2;
 DR HSP; Q29861; 1HSA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008955; P:immune response; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 FT NON TER 1
 SQ SEQUENCE 460 AA; 52263 MW; C1A0B6891978D93E CRC64;

Query Match 55.3%; Score 119; DB 2; Length 460;
 Best Local Similarity 100.0%; Pred. No. 8.1e-117; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWSAATVAQITQFYAEAEYAEAEFTYLEGCELELLRRYLENGKET 156
 DB 158 DGKDYISLNEDLSRWSAATVAQITQFYAEAEYAEAEFTYLEGCELELLRRYLENGKET 217

QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 218 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 276

RESULT 13
 Q860R0
 ID Q860R0 PRELIMINARY; PRT; 254 AA.
 AC Q860R0;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE MHC class Ib antigen.
 GN Name=HLA-F;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Y., He X., Xu L., Zeng Y.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY252371; AAO86775.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008955; P:immune response; IEA.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 SQ SEQUENCE 254 AA; 28588 MW; C81F225D409AAED2 CRC64;

Query Match 44.2%; Score 95; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 1.2e-91; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVXYDDTQTLRFDSDAIPRMBPFBFWBQEGPQWWTGYAKANAQTDRLVALNLL 60
 |||||

Db 44 IAVEYVDDTQFLRFPSDDAAIFRMEPREPWEQEGPQYWEWTGYAKANAQTDRAVLRNLL 103

QY 61 RRYNSEQAGSHTLQMGNGCDMPGDRLLRGYHQHA 95

Db 104 RRYNSEQAGSHTLQMGNGCDMPGDRLLRGYHQHA 138

RESULT 14

Q6ZUW0 PRELIMINARY; PRT; 349 AA.
AC Q6ZUW0;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Hypothetical protein FLJ43284.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125274; BAC86108.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; CI-set; 1.
DR DR Pfam; PF00047; IG; 1.
DR DR Pfam; PF00129; MHC I; 1.
DR DR Pfam; PF000050; MHC I; 1.
DR DR SMART; SM00407; IGcl; 1.
DR DR PROSITE; PS0835; IG_LIKE; 1.
DR DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;

Query Match 33.0%; Score 71; DB 2; Length 349;
Best Local Similarity 100.0%; Pred.No. 4.1e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LLRRYLENGKETLQADPPKARVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTO 204

Db 102 LLRRYLENGKETLQADPPKARVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTO 161

QY 205 DTELVEVTRPAG 215

Db 162 DTELVEVTRPAG 172

RESULT 15

BAC86108 PRELIMINARY; PRT; 349 AA.
AC BAC86108;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE CDNA FLJ43284 f1s, clone LYMP2000083, highly similar to HLA CLASS I
DE HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.,
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK125274; BAC86108.1;
SQ SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;

Query Match 33.0%; Score 71; DB 2; Length 349;
Best Local Similarity 100.0%; Pred.No. 4.1e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LLRRYLENGKETLQADPPKARVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTO 204

Db 102 LLRRYLENGKETLQADPPKARVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQTO 161

QY 205 DTELVEVTRPAG 215

Db 162 DTELVEVTRPAG 172

Search completed: December 15, 2004, 18:24:23
Job time : 112.677 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:13:46 / Search time 21.9836 Seconds
(without alignments)
941.000 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 215
Sequence: 1 LAVEYVDTQFLRFDSDAAL.....QRDGEETQDTLVELTRPAG 215

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	55.3	362	2 A60384	MHC class I histoc
2	70	32.6	345	2 S07114	MHC class I histoc
3	47	21.9	348	2 S29990	histocompatibility
4	43	20.0	316	2 C37028	MHC class I histoc
5	37	17.2	365	2 JH0544	class I histocompa
6	32	14.9	255	2 I54307	MHC HLA-A30US heav
7	32	14.9	274	2 I68774	MHC HLA-B39 chain
8	32	14.9	274	2 I54463	MHC HLA-B38 chain
9	32	14.9	274	2 S24439	class I histocompa
10	32	14.9	305	2 S07115	class I histocompa
11	32	14.9	308	2 I36956	MHC class I histoc
12	32	14.9	332	2 S06424	MHC HLA-B27-HS - h
13	32	14.9	338	2 I56116	MHC HLA-B71 - huma
14	32	14.9	350	2 I54308	MHC class I lympho
15	32	14.9	350	2 I68747	class I histocompa
16	32	14.9	354	2 S24433	class I histocompa
17	32	14.9	354	2 I59308	class I histocompa
18	32	14.9	354	2 I80166	class I histocompa
19	32	14.9	354	2 I80167	class I histocompa
20	32	14.9	354	2 I80165	class I histocompa
21	32	14.9	354	2 I80170	class I histocompa
22	32	14.9	354	2 I80168	class I histocompa
23	32	14.9	354	2 S24438	class I histocompa
24	32	14.9	354	2 S24440	class I histocompa
25	32	14.9	355	2 I80171	class I histocompa
26	32	14.9	355	2 I80169	class I histocompa
27	32	14.9	357	2 S11141	class I histocompa
28	32	14.9	358	2 S03538	class I histocompa
29	32	14.9	359	1 HLHUL2	MHC class I histoc

30 32 14.9 361 2 I54418
31 32 14.9 362 1 HLHUL0
32 32 14.9 362 1 HLHUB2
33 32 14.9 362 1 HLHUB7
34 32 14.9 362 2 JH0541
35 32 14.9 362 2 JH0539
36 32 14.9 362 2 JH0540
37 32 14.9 362 2 I36962
38 32 14.9 362 2 I56130
39 32 14.9 362 2 I84486
40 32 14.9 362 2 I62042
41 32 14.9 362 2 I37492
42 32 14.9 362 2 S52486
43 32 14.9 362 2 I38421
44 32 14.9 362 2 C35997
45 32 14.9 362 2 I56149

ALIGNMENTS

RESULT 1

A60384
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A60384; J0147
R:Kuray, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-537, 1990
A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.
A:Reference number: A60384; MUID:91197889; PMID:1707659
A:Accession: A60384
A:Molecule type: DNA
A:Residues: 1-362 <LUR>
A:Cross-references: UNIPROT:P30511
R:Geraghty, D.B.; Wei, X.; Orr, H.T.; Koller, B.H.
J. Exp. Med. 171, 1-18, 1990
A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I
A:Reference number: J0147; MUID:90111605; PMID:1688605
A:Accession: J0147
A:Molecule type: DNA
A:Residues: 1-362 <GER>
A:Cross-references: GB:X17093; NID:932223; PIDN:CAA34947.1; PID:g312407
A:Experimental source: lymphoblastoid cell line
C:Genetics:
A:Gene: GDB:HLA-F
A:Cross-references: GDB:125714
A:Map position: 6p21.3-6p21.3
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-111/Domain: alpha-1 <AL1>
F:78-104/Region: hypervariable
F:112-203/Domain: alpha-2 <AL2>
F:164-192/Region: hypervariable
F:204-295/Domain: alpha-3 <AL3>
F:217-282/Domain: immunoglobulin homology <IMM>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.3%; Score 119; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.8e-120; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISLNDLSWTAADTAQITQTFYEAEYAEFEFTYLEGECLELLRYLENGKET 156
DB 140 DGKDYISLNDLSWTAADTAQITQTFYEAEYAEFEFTYLEGECLELLRYLENGKET 199
QY 157 LQADPPKAVHAPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 215
DB 200 LQADPPKAVHAPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 258

RESULT 2

S07114
 MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S07114
 R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
 Nature 335, 268-271, 1988
 A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
 A:Reference number: S06424; MUID:86319000; PMID:3412487
 A:Accession: S07114
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-345 <LAW>
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: Glycoprotein; membrane protein
 F:1217-282/Domain: immunoglobulin homology <IMM>

Query Match 32.6%; Score 70; DB 2; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4.3e-67;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSWTAADTVAGITQRFYAEYAEFFTYLEGSCLELLRYLNGKET 156
 |||||
 DB 140 DGKDYISLNEDLSWTAADTVAGITQRFYAEYAEFFTYLEGSCLELLRYLNGKET 199
 |||||

QY 157 LQRADPPKAAH 166
 |||||
 DB 200 LQRADPPKAAH 209
 |||||

RESULT 3

S29990
 Histocompatibility antigen, HLA-F-like - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S29990
 R:Bontrop, R.R.
 Submitted to the EMBL Data Library, February 1993
 A:Reference number: S29990
 A:Accession: S29990
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-348 <BON>
 C:Cross-references: UNIPROT:P33617; EMBL:Z11819; NID:G38568; PIDN:CAA79885.1; PID:G38569
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:213-284/Domain: immunoglobulin homology <IMM>

Query Match 21.9%; Score 47; DB 2; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.5e-42;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ITQRFYAEYAEFFTYLEGSCLELLRYLNGKETLQRAADPPKAAH 166
 |||||
 DB 165 ITQRFYAEYAEFFTYLEGSCLELLRYLNGKETLQRAADPPKAAH 211
 |||||

RESULT 4

C37028
 MHC class I histocompatibility antigen HLA-C (clone 9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 14-Feb-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
 C:Accession: C37028
 R:Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella
 Immunogenetics 29, 80-91, 1989
 A:Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of
 A:Reference number: A37028; MUID:89122144; PMID:2514713
 A:Accession: C37028
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-316 <CIA>
 A:Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q29987; UNIPROT:Q9MY34; UNIPROT:O19677; UNIP

C:Genetics:

A:Gene: GDB:HLA-C
 A:Cross-references: GDB:119311; OMIM:142840
 A:Map position: 6p21.3-6p21.3
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:170-235/Domain: immunoglobulin homology <IMM>

Query Match 20.0%; Score 43; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 4.6e-38;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 SDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 |||||
 DB 169 SDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 211
 |||||

RESULT 5

JH0544
 class I histocompatibility antigen heavy chain precursor - lowland gorilla
 C:Species: Gorilla gorilla gorilla (lowland gorilla)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JH0544; JH0543
 R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
 J. Exp. Med. 174, 1491-1509, 1991
 A:Title: Gorilla class I major histocompatibility complex alleles: comparison to human at
 A:Reference number: JH0534; MUID:92078860; PMID:11744581
 A:Accession: JH0544
 A:Molecule type: DNA
 A:Residues: 1-365 <LAW>
 A:Cross-references: UNIPROT:P30383; EMBL:X60250; NID:G22878; PIDN:CAA42802.1; PID:G22879
 A:Experimental source: EBV-transformed B cell
 A:Note: Gogo-C0102
 A:Accession: JH0543
 A:Molecule type: DNA
 A:Residues: 1-319, 'S', 321-365 <LA2>
 A:Cross-references: EMBL:X60252
 A:Experimental source: EBV-transformed B cell
 A:Note: Gogo-C0101
 A:Note: the authors translated the codon AGT for residue 320 as Val
 C:Genetics: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
 A:Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-365/Product: class I histocompatibility antigen heavy chain #status predicted <CLA>
 F:25-114/Domain: alpha-1 <AL1>
 F:115-206/Domain: alpha-2 <AL2>
 F:207-298/Domain: alpha-3 <AL3>
 F:220-285/Domain: immunoglobulin homology <IMM>
 F:299-365/Domain: intracellular #status predicted <INT>

Query Match 17.2%; Score 37; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.5e-31;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGEQTD 205
 |||||
 DB 215 HHPISDHEATLRCWALGFYPAEITLTWQDGEQTD 251
 |||||

RESULT 6

I54307
 MHC HLA-A30JS heavy chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I54307
 R:Choo, S.Y.; Starling, G.C.; Anasetti, C.; Hansen, J.A.
 Hum. Immunol. 36, 20-26, 1993
 A:Title: Selection of an unrelated donor for marrow transplantation facilitated by the m
 A:Reference number: I54307; MUID:93209813; PMID:8458735
 A:Accession: I54307
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-255 <RES>
 A:Cross-references: GB:M93657; NID:G184155; PIDN:AAA58650.1; PID:G553335
 C:Genetics:
 A:Gene: HLA-A30J5
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 14.9%; Score 32; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.7e-26;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 7
 I68774
 MHC HLA-B39 chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C:Accession: I68774
 R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
 Immunogenetics 30, 200-207, 1989
 A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificity
 A:Reference number: I54463; MUID:89379286; PMID:2777338
 A:Accession: I68774
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-274 <RES>
 A:Cross-references: UNIPROT:Q29937; GB:M29865; NID:G187676; PIDN:AAA36223.1; PID:G187677
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 8
 I54463
 MHC HLA-B38 chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C:Accession: I54463
 R:Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
 Immunogenetics 30, 200-207, 1989
 A:Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificity
 A:Reference number: I54463; MUID:89379286; PMID:2777338
 A:Accession: I54463
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-274 <RES>
 A:Cross-references: UNIPROT:Q95365; GB:M29864; NID:G187674; PIDN:AAA36222.1; PID:G187675
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 9
 S24439
 Class I histocompatibility antigen HLA-B-3901 - human (fragment)
 C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C:Accession: S24439
 R:Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe
 Nature 357, 329-333, 1992
 A:Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
 A:Reference number: S24027; MUID:92269956; PMID:1589035
 A:Accession: S24439
 A:Molecule type: mRNA
 A:Residues: 1-274 <WAT>
 A:Cross-references: UNIPROT:Q96DW9; UNIPROT:Q8WLS2; UNIPROT:O19790; UNIPROT:Q95351; UNIP
 PROT:Q78218; UNIPROT:Q29653; UNIPROT:Q29657; UNIPROT:Q29654; UNIPROT:Q29655; UNIPROT:Q08
 U994; UNIPROT:Q951E7; UNIPROT:Q95346
 C:Genetics:
 A:Gene: HLA-B-3901
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: glycoprotein
 F:1-374/Product: Class I histocompatibility antigen HLA-B-3901 #status predicted <WAT>
 F:1-90/Domain: alpha-1 #status predicted <EX1>
 F:91-182/Domain: alpha-2 #status predicted <EX2>
 F:196-261/Domain: immunoglobulin homology <IMM>
 F:186-Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:101-164-Binding site: disulfide bonds: #status predicted

Query Match 14.9%; Score 32; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 2.8e-26;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
 DB 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222

RESULT 10
 S07115
 Class I histocompatibility antigen Ch18 alpha chain - chimpanzee (fragment)
 N:Alternate names: MHC Ch18 chain
 C:Species: Pan troglodytes (Chimpanzee)
 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
 C:Accession: S07115; I36960
 R:Lawlor, D.A.; Ward, F.B.; Ennis, P.D.; Jackson, A.P.; Parham, P.
 Nature 335, 268-271, 1988
 A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
 A:Reference number: S06424; MUID:88319000; PMID:3412487
 A:Accession: S07115
 A:Molecule type: mRNA
 A:Residues: 1-305 <LAW>
 A:Cross-references: UNIPROT:Q30991
 R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
 J. Immunol. 142, 3937-3950, 1989
 A:Title: Diversity and diversification of HLA-A,B,C alleles.
 A:Reference number: I36956; MUID:89235215; PMID:2715640
 A:Accession: I36960
 A:Molecule type: mRNA
 A:Residues: 1-305 <RES>
 A:Cross-references: GB:M24048; NID:G176820; PIDN:AAA35427.1; PID:G176821
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein
 F:58-149/Domain: alpha-2 #status predicted <EX2>
 F:163-228/Domain: immunoglobulin homology <IMM>
 F:250-274/Domain: transmembrane #status predicted <TM>
 F:275-305/Domain: intracellular #status predicted <INT>
 F:53-Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:168-131,170-226/Bisulfide bonds: #status predicted

Query Match 14.9%; Score 32; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 3.1e-26;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
 DB 158 HHPISDHEATLRCWALGFYPAEITLTWQDGE 189

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56116
R:Choo, S.Y.; Fan, L.A.; Hansen, J.A.
J. Immunol. 147, 174-180, 1991
A:Title: A novel HLA-B*27 allele maps B27 allotype specificity to the region around position 70
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:196-261/Domain: immunoglobulin homology <IMM>

A:Reference number: I56116; MUID:91268545; PMID:1711072
A:Accession: I56116
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-338 <RES>
A:Cross-references: UNIPROT:P03989; GB:M62852; NID:g187760; PIDN:AAA59647.1; PID:g187761
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:196-261/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 338;
Best Local Similarity 100.0%; Pred.No. 3.4e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATRCWALGFYPAEITLTWORDGE 200
DB 191 HHPISDHEATRCWALGFYPAEITLTWORDGE 222
|||||

RESULT 14

I54308 MHC HLA B71 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I54308
R:Rodriguez, S.G.; Johnson, A.H.; Hurlley, C.K.
Hum. Immunol. 37, 192-194, 1993
A:Title: Molecular characterization of HLA-B*71 from an African American individual.
A:Reference number: I54308; MUID:94064392; PMID:8244782
A:Accession: I54308
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-350 <RES>
A:Cross-references: UNIPROT:Q08173; GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237
C:Genetics:
A:Gene: GDB:HLA-B
A:Cross-references: GDB:120048; OMIM:142830
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 350;
Best Local Similarity 100.0%; Pred.No. 3.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATRCWALGFYPAEITLTWORDGE 200
DB 215 HHPISDHEATRCWALGFYPAEITLTWORDGE 246
|||||

RESULT 15

I68747 MHC class I lymphocyte antigen - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I68747
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B*8
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

A:Reference number: I54457; MUID:892333295; PMID:2714852
A:Accession: I68747
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-350 <RES>
A:Cross-references: UNIPROT:O19691; GB:M28204; NID:g576472; PIDN:AAA53257.1; PID:g576473
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:208-273/Domain: immunoglobulin homology <IMM>

Query Match 14.9%; Score 32; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 3.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db 203 HHPISDHEATLRCWALGFYPAEITLTWORDGE 234

Search completed: December 15, 2004, 18:25:18
Job time : 22.9836 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	215	100.0	215	11	US-09-819-371-6	Sequence 6, Appli
2	219	55.3	271	9	US-09-925-301-1431	Sequence 1431, Ap
3	119	55.3	274	11	US-09-819-371-5	Sequence 5, Appli
4	119	55.3	362	14	US-10-257-021-82	Sequence 82, Appli
5	119	55.3	442	16	US-10-408-765A-1887	Sequence 1887, Ap
6	95	44.2	362	11	US-09-819-371-4	Sequence 4, Appli
7	55	25.6	96	14	US-10-029-386-30718	Sequence 30718, A
8	52	24.2	186	15	US-10-264-049-4063	Sequence 4063, A
9	32	14.9	91	9	US-09-864-761-35461	Sequence 35461, A
10	32	14.9	110	9	US-09-796-652-799	Sequence 799, App
11	32	14.9	110	9	US-09-796-652-2139	Sequence 2139, Ap
12	32	14.9	110	14	US-10-040-862-799	Sequence 799, App
13	32	14.9	110	14	US-10-040-862-2139	Sequence 2139, App

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Db 181 CWAAGFYPAEITLTWQDGEQQTDTLVEVTRPAG 215
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RESULT 2
US-09-925-301-1431
; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431

Query Match 55.3%; Score 119; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156
Db 146 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 205
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 215
Db 206 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 264

RESULT 3
US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match 55.3%; Score 119; DB 11; Length 274;
Best Local Similarity 100.0%; Pred. No. 2e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156
Db 119 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 178
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 215
Db 179 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 237

RESULT 4
US-10-257-021-82
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; Sequence 82, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

Query Match 55.3%; Score 119; DB 14; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.5e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 199
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 215
Db 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 258

RESULT 5
US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Robin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1887

Query Match 55.3%; Score 119; DB 16; Length 442;
Best Local Similarity 100.0%; Pred. No. 3e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRWTAADTVAQITQFYEAEEYAEAEFRTYLEGCELLRRYLENGKET 199
QY 157 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 215
Db 200 LQADPPKAAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDTLVEVTRPAG 258
```

RESULT 6

US-09-819-371-4
; Sequence 4, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

Query Match 44.2%; Score 95; DB 11; Length 362;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAVEVDDTQFLRDSDAIAPRMPREPWVEQGPQYWEWTTGYAKANACTDRVALRNL 60

Db 44 TAVEVDDTQFLRDSDAIAPRMPREPWVEQGPQYWEWTTGYAKANACTDRVALRNL 103

QY 61 RYNOSEAGSHTLQGMGNDGPDGRLRLRGYQHA 95

Db 104 RYNOSEAGSHTLQGMGNDGPDGRLRLRGYQHA 138

RESULT 7

US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALU 2.00e-52
US-10-029-386-30718

Query Match 25.6%; Score 55; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.5e-46;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 DPPKAVAHPIISDEATRCWALGFYPAETITLWQDGEQTDVETREAG 215

Db 2 DPPKAVAHPIISDEATRCWALGFYPAETITLWQDGEQTDVETREAG 56

RESULT 8

US-10-264-049-4063
; Sequence 4063, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:

Query Match 24.2%; Score 52; DB 15; Length 186;

Best Local Similarity 100.0%; Pred. No. 1.1e-42;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4063
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (166)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (146)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (176)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4063

QY 44 YAKANAQTRVALRNLRRNQSEAGSHLTQGNMGCDMGDFGRLLRGVHQHA 95
 DB 1 YAKANAQTRVALRNLRRNQSEAGSHLTQGNMGCDMGDFGRLLRGVHQHA 52

RESULT 9
 US-09-864-761-35461
 ; Sequence 35461, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Weisheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aescmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-23
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 35461
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
 ; OTHER INFORMATION: EXPRESSED IN HELA00, SIGNAL = 53
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 47
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 32
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 58
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
 ; OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 8
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11

; OTHER INFORMATION: EST_HUMAN HIT: AW820291.1, EVALUE 3.00e-52
 ; OTHER INFORMATION: SWISSPROT HIT: P30487, EVALUE 3.00e-53
 US-09-864-761-35461

Query Match 14.9%; Score 32; DB 9; Length 91;
 Best Local Similarity 100.0%; Pred.No. 2.6e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
 DB 8 HHPISDHEATLRCWALGFYPAEITLTWORDGE 39

RESULT 10
 US-09-796-692-799
 ; Sequence 799, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannion, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 ; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
 ; FILE REFERENCE: 2077.001200
 ; CURRENT APPLICATION NUMBER: US/09/796,692
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 799
 ; LENGTH: 110
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-796-692-799

Query Match 14.9%; Score 32; DB 9; Length 110;
 Best Local Similarity 100.0%; Pred.No. 3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
 DB 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 11
 US-09-796-692-2139
 ; Sequence 2139, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander

```
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077, 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2139

Query Match      14.9%; Score 32; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 12
US-10-040-862-799
; Sequence 799, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
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; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-799

Query Match      14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 13
US-10-040-862-2139
; Sequence 2139, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
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; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-2139

Query Match 14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFPAEITLTWQDGE 200
|||||
Db 67 HHPISDHEATLRCWALGFPAEITLTWQDGE 98
|||||

RESULT 14
US-10-057-475B-799
; Sequence 799, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-799

Query Match 14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFPAEITLTWQDGE 200
|||||
Db 67 HHPISDHEATLRCWALGFPAEITLTWQDGE 98
|||||

RESULT 15
US-10-057-475B-2139
; Sequence 2139, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10379
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-2139

Query Match 14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDHEATLRCWALGFPAEITLTWQDGE 200
|||||
Db 67 HHPISDHEATLRCWALGFPAEITLTWQDGE 98
|||||

Search completed: December 15, 2004, 18:41:49
Job time : 88.4949 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:14:01 ; Search time 24.182 Seconds
(without alignments)
589.627 Million cell updates/sec

Title: US-09-819-371-6

Perfect score: 215

Sequence: 1 IAVEYVDDTQFLRDSAAI.....CRDGEHQDTQLVETRPAG 215

Scoring table:

Gapop 60.0 ; Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	35.8	120	4	US-09-513-999C-4290
2	32	14.9	274	1	US-08-222-851-1
3	17	7.9	184	3	US-09-153-586-21
4	16	7.4	117	2	US-08-406-057-9
5	16	7.4	117	2	US-08-958-316-9
6	16	7.4	145	2	US-08-406-057-8
7	16	7.4	145	3	US-08-958-316-8
8	16	7.4	361	3	US-08-652-265-22
9	16	7.4	361	3	US-08-834-497A-22
10	16	7.4	361	3	US-09-503-444A-22
11	15	7.0	92	4	US-09-673-809-25
12	15	7.0	182	1	US-08-127-954-135
13	15	7.0	182	1	US-08-127-954-151
14	15	7.0	274	2	US-08-484-905-105
15	15	7.0	274	2	US-08-484-905-106
16	15	7.0	274	2	US-08-484-905-107
17	15	7.0	274	2	US-08-484-905-108
18	15	7.0	274	3	US-08-481-985B-105
19	15	7.0	274	3	US-08-481-985B-106
20	15	7.0	274	3	US-08-481-985B-107
21	15	7.0	274	3	US-08-481-985B-108
22	15	7.0	274	3	US-08-370-476-105
23	15	7.0	274	3	US-08-370-476-106
24	15	7.0	274	3	US-08-370-476-107
25	15	7.0	274	3	US-08-370-476-108
26	15	7.0	341	3	US-08-890-719-38
27	15	7.0	365	2	US-08-484-905-97

Sequence 98, Appl
Sequence 99, Appl
Sequence 100, Appl
Sequence 101, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 97, Appl
Sequence 98, Appl
Sequence 99, Appl
Sequence 100, Appl
Sequence 101, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 97, Appl

365 2 US-08-484-905-98
365 2 US-08-484-905-99
365 2 US-08-484-905-100
365 2 US-08-484-905-101
365 2 US-08-484-905-102
365 2 US-08-484-905-103
365 2 US-08-484-905-104
365 3 US-08-481-985B-97
365 3 US-08-481-985B-98
365 3 US-08-481-985B-99
365 3 US-08-481-985B-100
365 3 US-08-481-985B-101
365 3 US-08-481-985B-102
365 3 US-08-481-985B-103
365 3 US-08-481-985B-104
365 3 US-08-652-265-23
365 3 US-08-834-497A-23
365 3 US-08-370-476-97

ALIGNMENTS

RESULT 1

US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLLLLSGALALT/DT
US-09-513-999C-4290

Query Match 35.8%; Score 77; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e-69;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IAVEYVDDTQFLRDSAAI PRMPEPWEQSGPQWETTCYAKANAQTDVALRNLL 60
DB 44 IAVEYVDDTQFLRDSAAI PRMPEPWEQSGPQWETTCYAKANAQTDVALRNLL 103

QY 61 RRYNQSEAGSHTLQGMN 77

DB 104 RRYNQSEAGSHTLQGMN 120

RESULT 2

US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128

; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")

;; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES

;; NUMBER OF SEQUENCES: 43

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: MORRISON & FOERSTER

;; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500

;; CITY: WASHINGTON

;; STATE: DC

;; COUNTRY: USA

;; ZIP: 20006-1812

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/222,851

;; FILING DATE: 05-APR-1994

;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:

;; NAME: MILLMAN, ROBERT A.

;; REGISTRATION NUMBER: 36,217

;; REFERENCE/DOCKET NUMBER: 28600-20200.22

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 887-1500

;; TELEFAX: (202) 494-0792

;; TELEX: 90-4030 MRSNFOERSH

;; INFORMATION FOR SEQ ID NO. 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 274 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; US-08-222-851-1

Query Match 14.9%; Score 32; DB 1; Length 274;

Best Local Similarity 100.0%; Pred. No. 5.7e-24; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 HHPISDEATLRCAWLGFPYPAETLTWQDGE 200

Db 191 HHPISDEATLRCAWLGFPYPAETLTWQDGE 222

RESULT 3

US-09-153-586-21

;; Sequence 21, Application US/09153586A

;; Patent No. 6270772

;; GENERAL INFORMATION:

;; APPLICANT: Burrows et al.

;; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of

;; FILE REFERENCE: 48823

;; CURRENT APPLICATION NUMBER: US/09/153,586A

;; CURRENT FILING DATE: 1998-09-15

;; EARLIER APPLICATION NUMBER: 60/064,552

;; EARLIER FILING DATE: 1997-09-16

;; EARLIER APPLICATION NUMBER: 60/064,555

;; EARLIER FILING DATE: 1997-10-10

;; NUMBER OF SEQ ID NOS: 30

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 21

;; LENGTH: 184

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-153-586-21

Query Match 7.9%; Score 17; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 3.9e-09; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 LRRYLENGKETLQRADP 162

Db 168 LRRYLENGKETLQRADP 184

RESULT 4

US-08-406-057-9

;; Sequence 9, Application US/08406057

;; Patent No. 5856442

;; GENERAL INFORMATION:

;; APPLICANT: CAROSELLA, EDGARDO D

;; APPLICANT: MOREAU, PHILIPPE

;; APPLICANT: GLUCKMAN, ELIANE

;; APPLICANT: KIRSZENBAUM, MAREK

;; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

;; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

;; CITY: ARLINGTON

;; STATE: VIRGINIA

;; COUNTRY: USA

;; ZIP: 2202

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Tape

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/406,057

;; FILING DATE: 17-MAR-1995

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PR 94 03179

;; FILING DATE: 18-MAR-1994

;; ATTORNEY/AGENT INFORMATION:

;; NAME: OBLON, NORVAN F

;; REGISTRATION NUMBER: 24,618

;; REFERENCE/DOCKET NUMBER: 846-331-0

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (703) 413-3000

;; TELEFAX: (703) 413-2220

;; TELEX: 248855 OPAT UR

;; INFORMATION FOR SEQ ID NO: 9:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 117 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-406-057-9

Query Match 7.4%; Score 16; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.6e-08; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 EATLRCAWLGFPYPAEI 191

Db 20 EATLRCAWLGFPYPAEI 35

RESULT 5

US-08-958-316-9

;; Sequence 9, Application US/08958316

;; Patent No. 6291659

;; GENERAL INFORMATION:

;; APPLICANT: CAROSELLA, EDGARDO D

;; APPLICANT: MOREAU, PHILIPPE

;; APPLICANT: GLUCKMAN, ELIANE

;; APPLICANT: KIRSZENBAUM, MAREK

;; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

;; NUMBER OF SEQUENCES: 17

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-958-316-9

Query Match 7.4%; Score 16; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
|||||

Db 20 EATLRCWALGFYPAEI 35

RESULT 6
US-08-406-057-8
Sequence 8, Application US/08406057
Patent No. 5856442
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIJANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-057-8

Query Match 7.4%; Score 16; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
|||||

Db 48 EATLRCWALGFYPAEI 63

RESULT 7
US-08-958-316-8
Sequence 8, Application US/08958316
Patent No. 6291659
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIJANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-958-316-8

Query Match 7.4%; Score 16; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
 |||||
 Db 48 EATLRCWALGFYPAEI 63

RESULT 8

US-08-652-265-22
 ; Sequence 22, Application US/08652265

; Patent No. 6025130

; GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.

; APPLICANT: Drayna, Dennis T.

; APPLICANT: Feder, John N.

; APPLICANT: Gnirke, Andreas

; APPLICANT: Ruddy, David

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Hereditary Hemochromatosis Gene

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,265

; FILING DATE: 23-MAY-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 17957-000500

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 361 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..361

; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"

US-08-652-265-22

Query Match 7.4%; Score 16; DB 3; Length 361;
 Best Local Similarity 100.0%; Pred. No. 7.2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
 |||||
 Db 222 EATLRCWALGFYPAEI 237

RESULT 9

US-08-934-497A-22

; Sequence 22, Application US/08934497A

; Patent No. 6140305

; GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.

; APPLICANT: Drayna, Dennis T.

; APPLICANT: Feder, John N.

; APPLICANT: Gnirke, Andreas

; APPLICANT: Ruddy, David

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,497A

; FILING DATE: 04-APR-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/652,265

; FILING DATE: 23-MAY-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/632,673

; FILING DATE: 16-APR-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,912

; FILING DATE: 04-APR-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Poissant, Brian M.

; REGISTRATION NUMBER: 28,462

; REFERENCE/DOCKET NUMBER: 8907-0056-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 361 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..361

; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"

US-08-834-497A-22

Query Match 7.4%; Score 16; DB 3; Length 361;
 Best Local Similarity 100.0%; Pred. No. 7.2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
 |||||
 Db 222 EATLRCWALGFYPAEI 237

RESULT 10

US-09-503-444A-22

; Sequence 22, Application US/09503444A

; Patent No. 6228594

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; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchihasi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..361
; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
US-09-503-444A-22

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Query Match          7.4%; Score 16; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 176 EATLRCWALGFYPAP1 191
DB 222 EATLRCWALGFYPAP1 237

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RESULT 11
US-09-673-809-25
; Sequence 25, Application US/09673809
; Patent No. 6528261
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA

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; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-25

Query Match          7.0%; Score 15; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LRRYLENGKETLQRA 160
DB 78 LRRYLENGKETLQRA 92

RESULT 12
US-08-127-954-135
; Sequence 135, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-135

```

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Query Match          7.0%; Score 15; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LRRYLENGKETLQRA 160
DB 168 LRRYLENGKETLQRA 182

```

```

RESULT 13
US-08-127-954-151
; Sequence 151, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-151

Query Match 7.0%; Score 15; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LRRYLENGKETLQRA 160
DB 168 LRRYLENGKETLQRA 182

RESULT 14
US-08-484-905-105
; Sequence 105, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-105

Query Match 7.0%; Score 15; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 FYPAEITLTWQDGE 200
DB 208 FYPAEITLTWQDGE 222

RESULT 15
US-08-484-905-106
; Sequence 106, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk

```

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; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-106

```

```

Query Match      7.0%; Score 15; DB 2; Length 274;
Best Local Similarity 100.0%; Pred.No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      186 FYPAEITLTWORDGE 200
          |||||
Db      208 FYPAEITLTWORDGE 222

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Search completed: December 15, 2004, 18:26:19
Job time : 25.182 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:00 ; Search time 95.8487 Seconds
(without alignments)
804.673 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 215
Sequence: 1 TAVEYVDITQLRFDSDAAI.....QRDGEQTQDTLVELTRPAG 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq 23Sep04: *
1: Genesep1980s: *
2: Genesep1990s: *
3: Genesep2000s: *
4: Genesep2001s: *
5: Genesep2002s: *
6: Genesep2003as: *
7: Genesep2003bs: *
8: Genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	55.3	215	4	AAG64619 Human can
2	119	55.3	215	7	ADP55589
3	119	55.3	271	3	AB43986 Human can
4	119	55.3	274	4	AAG64618 Human can
5	119	55.3	274	7	ADP55588
6	119	55.3	362	4	AAG64617 Human can
7	119	55.3	362	4	AB550296 HLA-Cw ov
8	119	55.3	362	7	ADP55587 Human can
9	119	55.3	362	8	ADP55587
10	119	55.3	362	8	ADP12500 Protein e
11	119	55.3	442	7	ADU70081 Human hea
12	119	55.3	677	4	ABG26726 Novel hum
13	77	35.8	120	3	AG000209 Human sec
14	55	25.6	96	8	AB057084 Human gen
15	52	24.2	186	5	ABP42931 Human ova
16	32	14.9	91	4	AA115751 Peptide #
17	32	14.9	91	4	AA115751 Peptide #
18	32	14.9	91	4	AB34748 Peptide #
19	32	14.9	91	4	AB28260 Peptide #
20	32	14.9	91	4	AB28260 Peptide #
21	32	14.9	91	4	AB28260 Peptide #
22	32	14.9	91	4	AB28260 Peptide #
23	32	14.9	91	4	AB28260 Peptide #
24	32	14.9	91	4	AB28260 Peptide #
25	32	14.9	91	5	ABG37468 Human pep

Aam81775 Human hae
Aam80435 Human hae
Aaol0522 Human pol
Abt58386 Human NOV
Abp42373 Human ova
Aap80911 Consensus
Adf69111 Human lun
Aam23760 Human EST
Aap70590 Sequence
Aap70155 Sequence
Adp55319 Human mhc
Adp75476 Marker ge
Adp12599 Protein e
Adp12521 Protein e
Aau32882 Novel hum
Aa006772 Human pol
Aas58497 Lung canc
Adh48788 NOV31 pro
Ade40250 Human NOV
AB057455 Human gen

ALIGNMENTS

RESULT 1
AAG64619
ID AAG64619 standard; protein; 215 AA.
XX
AC AAG64619;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cancer cell specific HLA-F antigen SEQ ID 6.
XX
KW HLA-F antigen; cancer cell specific; human.
XX
OS Homo sapiens.
XX
PN JP2001095584-A.
XX
PD 10-APR-2001.
XX
PF 30-SEP-1999; 99JP-00279566.
XX
PR 30-SEP-1999; 99JP-00279566.
XX
PA (EGAW//) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU//) KIMURA K.
XX
DR WPI; 2001-360493/38.
DR N-PSDB; AAH45557.
XX
PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
PS Claim 1; Page 11-12; 12pp; Japanese.
XX
CC This invention relates to a cancer cell specific HLA-F antigen. The
CC invention includes DNA encoding the antigen, and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
XX invention
XX
SQ Sequence 215 AA;

Query Match 55.3%; Score 119; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.4e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISINEDLRGWTAAATVAQITQRFVAAEYAEFRNYLEGECLLELLRYLENGKET 156

Db 97 DGRDYISLNEDLSRWSAATVAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156
 QY 157 LQADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215
 Db 157 LQADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215

RESULT 2

ADFS5589
 ID ADFS5589 standard; protein; 215 AA.
 AC ADFS5589;
 XX
 DT 12-FEB-2004 (first entry)
 DE Fragment #2 of human cancer-cell specific HLA-F antigen.
 KW Cancer; human leukocyte antigen-F; HLA-F;
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 KW major histocompatibility complex; MHC; cancer cell; human.
 OS Homo sapiens.
 XX
 PN JP2003012544-A.
 PD 15-JAN-2003.
 XX
 PF 27-MAR-2002; 2002JP-00089991.
 XX
 PR 27-MAR-2001; 2001JP-00090121.
 XX
 PA (EGAWA/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA Y.
 XX
 DR WPI; 2003-486263/46.
 DR N-PSDB; ADFS5586.
 XX
 PT Agent for preventing and treating cancer, comprising human leukocyte
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 XX
 PS Claim 7; SEQ ID NO 6; 19pp; Japanese.
 CC The present invention relates to an agent for preventing or treating
 CC cancer. The agent comprises a portion or a complete sequence of a human
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is
 CC unrestricted to the major histocompatibility complex (MHC) and specific
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
 CC is useful for treating or preventing cancer. A cell capable of presenting
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
 CC for diagnosing cancer. The present sequence represents part of the human
 CC cancer-cell specific HLA-F antigen.
 XX
 SQ Sequence 215 AA;
 Query Match 55.3%; Score 119; DB 7; Length 215;
 Best Local Similarity 100.0%; Pred. No. 3.4e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGRDYISLNEDLSRWSAATVAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156
 Db 97 DGRDYISLNEDLSRWSAATVAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156
 QY 157 LQADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215
 Db 157 LQADPPKAHVHPISDHEATLRCWALGFYPAEITLTWQDGEQOTDELVEPTRAG 215

RESULT 3

AAB43986
 ID AAB43986 standard; protein; 271 AA.
 XX
 AC AAB43986;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human cancer associated protein sequence SEQ ID NO:1431.
 XX
 KW Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;
 KW dermatological; neuroprotective; thrombolytic; coagulant; neotropic;
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ rejection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.
 OS Homo sapiens.
 XX
 PN WO200055350-A1.
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005882.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587533/55.
 DR N-PSDB; AAB43985.
 XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer.
 XX
 PS Claim 11; Page 2115-2116; 2352pp; English.
 XX
 CC AAB77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43986 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnary; immunomodulator;
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; coagulant;
 CC dermatological; neuroprotective; cardiac; thrombolytic; antipsoriatic;
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 271 AA;
 Query Match 55.3%; Score 119; DB 3; Length 271;
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGRDYISLNEDLSRWSAATVAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 156
 Db 146 DGRDYISLNEDLSRWSAATVAQITQFYAEAEYAEFFTYLEGCELELLRRYLENGKET 205

QY 157 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 206 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 264

RESULT 4

AAG64618
 ID AAG64618 standard; protein; 274 AA.

AC AAG64618;
 DT 12-SEP-2001 (first entry)
 DE Human cancer cell specific HLA-F antigen SEQ ID 5.
 KW HLA-F antigen; cancer cell specific; human.

OS Homo sapiens.

PN JP2001095584-A.

PD 10-APR-2001

PF 30-SEP-1999; 99JP-00279566.

PR 30-SEP-1999; 99JP-00279566.

PA (EGAW//) EGAWA K.

PA (MEDI-) MEDINET KK.

PA (KIMU//) KIMURA Y.

DR WPI; 2001-360493/38.

DR N-PSDB; AAF45556.

PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.

PS Claim 2; Page 10-11; 12pp; Japanese.

CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX Sequence 274 AA;

Query Match 55.3%; Score 119; DB 4; Length 274;
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEILRSWTAADTVAQITQRYEAEYAEFFRYLSEGCLELLRRYLENGKET 156
 DB 119 DGKDYISLNEILRSWTAADTVAQITQRYEAEYAEFFRYLSEGCLELLRRYLENGKET 178

QY 157 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 179 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 237

RESULT 5

ADF55588
 ID ADF55588 standard; protein; 274 AA.

AC ADF55588;
 DT 12-FEB-2004 (first entry)
 DE Fragment #1 of human cancer-cell specific HLA-F antigen.
 KW Cancer; human leukocyte antigen-F; HLA-F;

KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 KW major histocompatibility complex; MHC; cancer cell; human.

OS Homo sapiens.

PN JP2003012544-A.

PD 15-JAN-2003.

PF 27-MAR-2002; 2002JP-00088991.

PR 27-MAR-2001; 2001JP-00090121.

PA (EGAW//) EGAWA K.

PA (MEDI-) MEDINET KK.

PA (KIMU//) KIMURA Y.

DR WPI; 2003-486263/46.

DR N-PSDB; ADF55585.

PT Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.

PS Claim 7; SEQ ID NO 5; 19pp; Japanese.

CC The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HLA-F antigen.

XX Sequence 274 AA;

Query Match 55.3%; Score 119; DB 7; Length 274;
 Best Local Similarity 100.0%; Pred. No. 4.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEILRSWTAADTVAQITQRYEAEYAEFFRYLSEGCLELLRRYLENGKET 156
 DB 119 DGKDYISLNEILRSWTAADTVAQITQRYEAEYAEFFRYLSEGCLELLRRYLENGKET 178

QY 157 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 215
 DB 179 LQRADPPKARVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVEVPAG 237

RESULT 6

AAG64617
 ID AAG64617 standard; protein; 362 AA.

AC AAG64617;

DT 12-SEP-2001 (first entry)

DE Human cancer cell specific HLA-F antigen SEQ ID 4.

KW HLA-F antigen; cancer cell specific; human.

OS Homo sapiens.

PN JP2001095584-A.

PD 10-APR-2001.

PF 30-SEP-1999; 99JP-00279566.

XX

PR 30-SEP-1999; 99JP-00279566.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA K.
 DR WPI; 2001-360493/38.
 DR N-PSDB; AAH45555.
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX Disclosure; Page 9-10; 12pp; Japanese.
 CC This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer, in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
 CC sequence represents the cancer cell-specific HLA-F antigen of the
 CC invention
 XX Sequence 362 AA;
 SQ
 Query Match 55.3%; Score 119; DB 4; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 156
 DB 140 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 199
 QY 157 LQRADPPKAAHVAHPISDHEATLRCWALGFYPFAEITLTWQDGEQTDTELVEIRPAG 215
 DB 200 LQRADPPKAAHVAHPISDHEATLRCWALGFYPFAEITLTWQDGEQTDTELVEIRPAG 258
 RESULT 7
 ABB50296
 ID ABB50296 standard; protein; 362 AA.
 AC ABB50296;
 XX
 DT 08-FEB-2002 (first entry)
 DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
 XX Ovarian tumour marker gene; human; overexpression; upregulation;
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
 KW identification; serous cystadenoma; borderline serous tumour;
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
 KW immune response pathway; cell proliferation regulation; protein folding;
 KW membrane localised; secreted; therapeutic target; cytostatic;
 KW gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200175177-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010947.
 XX
 PR 03-APR-2000; 2000US-0194336P.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
 DR WPI; 2001-626450/72.
 DR N-PSDB; ABA83122.

XX Detecting and identifying ovarian tumor, identifying increased risk for
 PT developing ovarian cancer, and determining effectiveness of ovarian
 PT cancer treatment, by measuring expression level of ovarian tumor marker
 PT gene.
 XX
 PS Claim 23; Page 126-127; 140pp; English.
 XX
 CC The invention relates to methods for diagnosing and prognosing ovarian
 CC tumors in an individual via the detection and measurement of the
 CC expression of ovarian tumor marker genes (ABA83081-ABA83122, ABA83180,
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
 CC ABA83181 and ABA83183). The methods of the invention are useful for
 CC detecting an ovarian tumor in a patient, for identifying an individual
 CC at increased risk for developing ovarian cancer, in prognostic tests for
 CC assessing the relative severity of ovarian cancer, in tests for
 CC monitoring a patient in remission from ovarian cancer and in tests for
 CC monitoring disease status in a patient being treated for ovarian cancer.
 CC The methods can additionally be used to identify a particular tumor as
 CC being an ovarian tumor (i.e., an epithelial ovarian tumor selected from
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
 CC tumour. The ovarian tumor marker genes of the invention were identified
 CC using SAGE (serial analysis of gene expression) and were found to be
 CC overexpressed in a broad variety of ovarian epithelial tumour cells
 CC relative to normal ovarian epithelial cells. The marker genes are
 CC implicated in immune response pathways, in the regulation of cell
 CC proliferation and in protein folding, and many of these are membrane-
 CC localised or secreted. In addition to their use as diagnostic and
 CC prognostic markers, the ovarian tumour marker genes or their encoded
 CC proteins may be used as therapeutic targets for the treatment and
 CC prevention of ovarian cancer. Sequences ABB50257-ABB50399 represent
 CC proteins encoded by ovarian tumour marker genes of the invention
 XX
 SQ Sequence 362 AA;
 Query Match 55.3%; Score 119; DB 4; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 156
 DB 140 DGKDYISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGCELELLRYLENGKET 199
 QY 157 LQRADPPKAAHVAHPISDHEATLRCWALGFYPFAEITLTWQDGEQTDTELVEIRPAG 215
 DB 200 LQRADPPKAAHVAHPISDHEATLRCWALGFYPFAEITLTWQDGEQTDTELVEIRPAG 258
 RESULT 8
 ADF55587
 ID ADF55587 standard; protein; 362 AA.
 AC ADF55587;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human cancer-cell specific HLA-F antigen.
 XX
 KW Cancer; human leukocyte antigen-F; HLA-F;
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 KW major histocompatibility complex; MHC; cancer cell; human.
 XX
 OS Homo sapiens.
 XX
 PN JP2003012544-A.
 XX
 PD 15-JAN-2003.
 XX
 PF 27-MAR-2002; 2002JP-00088991.
 XX

PR 27-MAR-2001; 2001JP-00090121.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA Y.
 XX WPI; 2003-486263/46.
 DR N-PSDB; ADF55384.
 XX
 XX Agent for preventing and treating cancer, comprising human leukocyte
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 XX
 XX Claim 5; SEQ ID NO 4; 19pp; Japanese.
 XX
 XX The present invention relates to an agent for preventing or treating
 CC cancer. The agent comprises a portion or a complete sequence of a human
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is
 CC unrestricted to the major histocompatibility complex (MHC) and specific
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
 CC is useful for treating or preventing cancer. A cell capable of presenting
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
 CC for diagnosing cancer. The present sequence represents human cancer-cell
 CC specific HLA-F antigen.
 XX
 XX Sequence 362 AA;
 SQ
 Query Match 55.3%; Score 119; DB 7; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 156
 DB 140 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 199
 QY 157 LQADPPKRAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215
 DB 200 LQADPPKRAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 259
 RESULT 9
 ADJ75372
 ID ADJ75372 standard; protein; 362 AA.
 XX
 AC ADJ75372;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:624.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 XX
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 XX (GENO-) GENOX RES INC.
 XX
 XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 PI WPI; 2004-193155/19.
 XX
 DR 2004-193155/19.

PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 XX Example 11; SEQ ID NO 624; 241pp; English.
 XX
 XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC the marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 362 AA;
 SQ
 Query Match 55.3%; Score 119; DB 8; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.1e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 156
 DB 140 DGKDYISLNEDLRSTAAADTVAQITQRFYAEAEVAFRTYLEGCELELLRRYLENGKET 199
 QY 157 LQADPPKRAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 215
 DB 200 LQADPPKRAHVAAHPISDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAG 258
 RESULT 10
 ADP12500
 ID ADP12500 standard; protein; 362 AA.
 XX
 AC ADP12500;
 XX
 XX 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #110.
 XX
 XX transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 XX

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PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00323899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 65; SEQ ID NO 2509; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
SQ Sequence 362 AA;
Query Match 55.3%; Score 119; DB 8; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.1e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFRYLEGCELLRRYLENGKET 156
DB 140 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFRYLEGCELLRRYLENGKET 199
QY 157 LQADPPKHAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQTDTELVEVPAG 215
DB 200 LQADPPKHAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQTDTELVEVPAG 258
RESULT 11
ID ADJ70081 standard; protein; 442 AA.
XX
AC ADJ70081;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target Segid1887.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.

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PR 17-JUN-2002; 2002US-038987P.
PR 20-SEP-2002; 2002US-0412418P.
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Faly ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1887; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 442 AA;
Query Match 55.3%; Score 119; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.1e-107;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFRYLEGCELLRRYLENGKET 156
DB 140 DGKDYISLNEDLSRWTAADTVQAQITQRFYEAEEYAEFFRYLEGCELLRRYLENGKET 199
QY 157 LQADPPKHAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQTDTELVEVPAG 215
DB 200 LQADPPKHAHVAHPISDHEATLRCWALGFGYPABITLTWQDGBEQTDTELVEVPAG 258
RESULT 12
ABG26726
ID ABG26726 standard; protein; 677 AA.
XX
AC ABG26726;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26717.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.

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(HYSE-) HYSEQ INC.
 Drmanac RT, Liu C, Tang YT;
 WPI; 2001-639362/73.
 N-PSDB; AAS90913.
 New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity.
 Claim 20; SEQ ID NO 57085; 103pp; English.
 The invention relates to isolated polynucleotide (I) and polypeptide (II)
 sequences. (I) is useful as hybridisation probes, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 of sites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activity. The
 polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. ASG00010-ABG030377 represent novel human diagnostic
 amino acid sequences of the invention. Note: the sequence data for this
 patent did not appear in the printed specification, but was obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 Sequence 677 AA;
 Query Match 55.3%; Score 119; DB 4; Length 677;
 Best Local Similarity 100.0%; Pred. No. 8.6e-107;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 DGDYISLNEDLRSTADTAQAQITQRYEAEVYAEAEFRVLEGECLLRVLENGKET 156
 DB 449 DGDYISLNEDLRSTADTAQAQITQRYEAEVYAEAEFRVLEGECLLRVLENGKET 508
 QY 157 LQADPPKAAHVAHHPISDHEATLRCWALGFYPAITLTWQDGEQDTLVEVTRPAG 215
 DB 509 LQADPPKAAHVAHHPISDHEATLRCWALGFYPAITLTWQDGEQDTLVEVTRPAG 567
 RESULT 13
 AAG00209
 ID AAG00209 standard; protein; 120 AA.
 XX
 AC AAG00209;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 4290.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 XX 26-FEB-1999; 99US-0122487P.
 (GEST) GENSET.
 Dumas Milne Edwards J, Duclert A, Giordano J;
 WPI; 2000-500381/45.
 DR N-PSDB; AAC00215.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 120 AA;
 Query Match 35.8%; Score 77; DB 3; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.4e-66;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IAVEYVDDTQFLRPSDAAIPRMEPRPWPVEQSGPQWETTGAKANAQTDRAVALNLL 60
 DB 44 IAVEYVDDTQFLRPSDAAIPRMEPRPWPVEQSGPQWETTGAKANAQTDRAVALNLL 103
 QY 61 RRYNQSEAGSHTLQGMN 77
 DB 104 RRYNQSEAGSHTLQGMN 120
 RESULT 14
 ABO57084
 ID ABO57084 standard; protein; 96 AA.
 XX
 AC ABO57084;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon protein #3318.
 XX
 KW Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 XX WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

PS Claim 45; SEQ ID NO 30718; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6988 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon. In assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe protein of the invention. Note: the sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC segdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 96 AA;

Query Match 25.6%; Score 55; DB 8; Length 96;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 DPPKHAHVHPISDHEATLRCWALGYPAPETITLWQDGEETQDTLVEVPAG 215

Db 2 DPPKHAHVHPISDHEATLRCWALGYPAPETITLWQDGEETQDTLVEVPAG 56

RESULT 15

ABP42931 standard; protein; 186 AA.

XX ABP42931;

XX 22-AUG-2002 (first entry)

DE Human ovarian antigen HPDRT37, SEQ ID NO:4063.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW Gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ56008.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 4063; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 186 AA;

Query Match 24.2%; Score 52; DB 5; Length 186;

Best Local Similarity 100.0%; Pred. No. 3.9e-42;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 YAKANAQTDVVALNRLRYNQSEAGSHTLQMGNCMDGPDGRLRLGYHOHA 95

Db 1 YAKANAQTDVVALNRLRYNQSEAGSHTLQMGNCMDGPDGRLRLGYHOHA 52

Search completed: December 15, 2004, 18:20:04

Job time : 97.8487 secs

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:30 ; Search time 142.323 seconds
(without alignments)
1107.709 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRYFSTAVSPGRGEP.....QRYTCHVQHGELPQLRLW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt.02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	274	100.0	324	2 Q861E9	Q861E9 homo sapien
2	274	100.0	324	2 Q861F0	Q861F0 homo sapien
3	274	100.0	346	2 Q8WLP5	Q8WLP5 homo sapien
4	274	100.0	346	2 Q6DU28	Q6DU28 homo sapien
5	274	100.0	346	2 A4H62991	A4H62991 homo sapi
6	274	100.0	362	1 HLA-F HUMAN	P30511 homo sapien
7	274	100.0	362	2 BAC54915	BAC54915 homo sapi
8	274	100.0	460	2 Q8SHC0	Q8SHC0 homo sapien
9	250	91.2	346	2 Q8MGQ1	Q8MGQ1 homo sapien
10	224	81.8	346	2 Q6DU20	Q6DU20 homo sapien
11	208	75.9	346	2 Q95IT2	Q95IT2 pan troglod
12	208	75.9	362	2 Q7YR27	Q7YR27 pan troglod
13	182	66.4	254	2 Q860R0	Q860R0 homo sapien
14	126	46.0	346	1 IC28 PANTR	P16215 pan troglod
15	108	39.4	349	2 Q8ZUM0	Q8ZUM0 homo sapien
16	108	39.4	349	2 BAC86108	BAC86108 homo sapi
17	87	31.8	91	2 Q7RPX7	Q7RPX7 gorilla gor
18	73	26.6	316	2 Q29958	Q29958 homo sapien
19	62	22.6	314	2 Q860F6	Q860F6 macaca mela
20	61	22.3	353	2 Q8MXS6	Q8MXS6 macaca mela
21	61	22.3	353	2 Q8MXS7	Q8MXS7 macaca mela
22	61	22.3	354	2 Q70UE5	Q70UE5 macaca mela
23	61	22.3	354	2 Q70UE6	Q70UE6 macaca mela
24	61	22.3	354	2 Q70UE7	Q70UE7 macaca mela
25	61	22.3	354	2 CAD65766	CAD65766 macaca mu
26	61	22.3	354	2 CAD65765	CAD65765 macaca mu
27	61	22.3	354	2 CAD65767	CAD65767 macaca mu
28	61	22.3	365	2 Q8MXS5	Q8MXS5 macaca mela
29	59	21.5	59	2 Q78094	Q78094 homo sapien
30	59	21.5	348	1 HLA-F MACMU	P33617 macaca mela
31	58	21.2	354	2 Q70SIO	Q70SIO macaca mela

RESULT 1

Q861E9	Q861E9	PRELIMINARY;	PRT;	324 AA.
AC	Q861E9			
DT	01-JUN-2003 (Tremblrel. 24, Created)			
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	MHC class I antigen (Fragment).			
GN	Name=HLA-F;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Liu Y., Xu L., Zeng Y., He X.;			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY221102; AAC34407.1; -.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG-cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR001039; MHC_I.			
DR	Pfam; PF07654; CI-set; 1.			
DR	Pfam; PF00129; MHC_I; 1.			
DR	PRINTS; PR01638; MHCCLASSI.			
DR	ProDom; PD000050; MHC_I; 1.			
DR	PROSITE; PS00835; IG_Like; 1.			
DR	PROSITE; PS00290; IG_MHC; 1.			
FT	NON_TER 1 324			
FT	NON_TER 324 324			
SQ	SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;			
Query Match	Best Local Similarity	100.0%;	Score 274;	DB 2; Length 324;
Matches 274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 GSHSLRYFSTAVSPGRGEPRIYAVEYVDTQFLRDSDAAI PRMFP RPFWVEQEGPQYW 60			
Db	18 GSHSLRYFSTAVSPGRGEPRIYAVEYVDTQFLRDSDAAI PRMFP RPFWVEQEGPQYW 77			
QY	61 EWTGYAKANAQTDRAVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 120			
Db	78 EWTGYAKANAQTDRAVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLRLRGYHQHAYDG 137			
QY	121 KDYSLSNEDLSWTAADTVAQITQRFYAEYAEAEERTYLEGCLLLRYLNGKETLIQ 180			
Db	138 KDYSLSNEDLSWTAADTVAQITQRFYAEYAEAEERTYLEGCLLLRYLNGKETLIQ 197			
QY	181 RADPPKAVHAPHSDEATLRCWALGFYPAETLTWQDGEQTQDTLVEFRPADGDT 240			
Db	198 RADPPKAVHAPHSDEATLRCWALGFYPAETLTWQDGEQTQDTLVEFRPADGDT 257			

32	58	21.2	354	2	CAD83073	Cad83073 macaca mu
33	58	21.2	365	2	Q617A3	Q617A3 macaca fasc
34	55	20.1	365	2	Q617A9	Q617A9 macaca fasc
35	53	19.3	354	2	Q70SH4	Q70SH4 macaca mula
36	53	19.3	354	2	CAD83079	Cad83079 macaca mu
37	53	19.3	355	2	Q767W6	Q767W6 aotus tri
38	53	19.3	355	2	BAD18842	BAD18842 aotus tri
39	53	19.3	365	2	Q61796	Q61796 macaca fasc
40	50	18.2	351	2	Q70PL7	Q70PL7 macaca mula
41	50	18.2	351	2	Q70PM0	Q70PM0 macaca mula
42	50	18.2	351	2	CAD89636	Cad89636 macaca mu
43	50	18.2	351	2	CAD89639	Cad89639 macaca mu
44	45	16.4	330	2	Q30713	Q30713 macaca mula
45	45	16.4	338	2	Q95510	Q95510 leopardus p

ALIGNMENTS

QY 241 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
 DB 258 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 2

Q861F0 PRELIMINARY; PRT; 324 AA.
 AC Q861F0;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Nonclassical MHC class I antigen (fragment).
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA He X., Xu L., Liu Y., Zeng Y.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY216682; AAC37689.1; -;
 DR HSSP; Q29961; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS00835; IGC_LIKE; 1.
 DR PROSITE; PS00290; IGC_VHC; 1.
 FT NON_TER 1 324
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D271654 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 3,3e-280;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRFTAVSRPGGEGRYTAVRYDDTQFLRFDSDAAIPRPEPWEQEGPOYW 60
 DB 18 GSHSLRFTAVSRPGGEGRYTAVRYDDTQFLRFDSDAAIPRPEPWEQEGPOYW 77
 QY 61 EWTGKAKANAQTDVALRNLRLRYNQSEAGSHTLQGNMGCDWGPDRLLRGYHQHAYDG 120
 DB 78 EWTGKAKANAQTDVALRNLRLRYNQSEAGSHTLQGNMGCDWGPDRLLRGYHQHAYDG 137
 QY 121 KQYISLNEEDRSWTAADTVAQITQRYEAEYAEERTYLEGECUELLRRYLENGKETLQ 180
 DB 138 KQYISLNEEDRSWTAADTVAQITQRYEAEYAEERTYLEGECUELLRRYLENGKETLQ 197
 QY 181 RADPPKAVAHPTSDHEATLRCWALGFYPAEITLTWQDGEQQTQELVETRPAGDGT 240
 DB 198 RADPPKAVAHPTSDHEATLRCWALGFYPAEITLTWQDGEQQTQELVETRPAGDGT 257
 QY 241 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
 DB 258 FQKAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291

RESULT 3

Q8WLP5 PRELIMINARY; PRT; 346 AA.
 AC Q8WLP5;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-OCT-2004 (TRENBLrel. 28, Last annotation update)

DE MHC class Ib antigen (HLA-F protein).
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA He X., Xu L., Liu Y., Zeng Y.;
 RT Identification of a novel HLA-F allele - HLA-F*010102.;
 RL Tissue Antigens 63:181-183(2004).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA He X., Xu L., Liu Y., Zeng Y.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Schmutz J., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Pvo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A5232385; RAM74980.1; -;
 DR EMBL; A5232387; RAM74982.1; -;
 DR EMBL; A5232388; RAM74983.1; -;
 DR EMBL; A5232389; RAM74984.1; -;
 DR EMBL; A5232390; RAM74985.1; -;
 DR EMBL; A5232393; RAM74988.1; -;
 DR EMBL; A5232394; RAM74989.1; -;
 DR EMBL; A5232395; RAM74990.1; -;
 DR EMBL; A5232396; RAM74991.1; -;
 DR EMBL; A5232397; RAM74992.1; -;
 DR EMBL; A5232398; RAM74993.1; -;
 DR EMBL; AY253270; AAO86773.1; -;
 DR EMBL; BC062991; AAH62991.1; -;
 DR EMBL; AY645742; RAT73225.1; -;
 DR EMBL; AY645743; RAT73226.1; -;
 DR EMBL; AY645744; RAT73227.1; -;
 DR EMBL; AY645745; RAT73228.1; -;
 DR EMBL; AY645746; RAT73229.1; -;
 DR EMBL; AY645749; RAT73232.1; -;
 DR EMBL; AY645750; RAT73233.1; -;

DR EMBL; AY645751; AAT73234.1; -
 DR EMBL; AY645752; AAT73235.1; -
 DR EMBL; AY645753; AAT73236.1; -
 DR EMBL; AY645756; AAT73239.1; -
 DR EMBL; AY645757; AAT73240.1; -
 DR EMBL; AY645758; AAT73241.1; -
 DR EMBL; AY645759; AAT73242.1; -
 DR EMBL; AF523286; AAT74981.1; -
 DR HSSP; Q29961; 1HSA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC I.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00129; MHC I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC I; 1.
 DR SMART; SM00407; ICcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Transmembrane.
 SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;
 Query Match 100.0%; Score 274; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.5e-280;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
 DB 22 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81
 QY 61 EWTTCYAKANAQTDVALNLLRRYNQSEAGSHTLQMGNGCDMPDGLRLRGVHQYADG 120
 DB 82 EWTTCYAKANAQTDVALNLLRRYNQSEAGSHTLQMGNGCDMPDGLRLRGVHQYADG 141
 QY 121 KDYISLNEDLSRWTAAADVAQITQRFYAEAEYAEERTVLEGECLLELLRYLNGKETLQ 180
 DB 142 KDYISLNEDLSRWTAAADVAQITQRFYAEAEYAEERTVLEGECLLELLRYLNGKETLQ 201
 QY 181 RADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVETRPAGDGT 240
 DB 202 RADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVETRPAGDGT 261
 QY 241 FOKWAAVVPVSGEEOQRYTCHVQHEGLPOPLILRW 274
 DB 262 FOKWAAVVPVSGEEOQRYTCHVQHEGLPOPLILRW 295
 RESULT 4
 Q6DU28 PRELIMINARY; PRT; 346 AA.
 AC Q6DU28;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE MHC class Ib antigen.
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY645747; AAT73230.1; -
 SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;
 Query Match 100.0%; Score 274; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.5e-280;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
 DB 22 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81
 QY 61 EWTTCYAKANAQTDVALNLLRRYNQSEAGSHTLQMGNGCDMPDGLRLRGVHQYADG 120
 DB 82 EWTTCYAKANAQTDVALNLLRRYNQSEAGSHTLQMGNGCDMPDGLRLRGVHQYADG 141
 QY 121 KDYISLNEDLSRWTAAADVAQITQRFYAEAEYAEERTVLEGECLLELLRYLNGKETLQ 180
 DB 142 KDYISLNEDLSRWTAAADVAQITQRFYAEAEYAEERTVLEGECLLELLRYLNGKETLQ 201
 QY 181 RADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVETRPAGDGT 240
 DB 202 RADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEOQTDELVETRPAGDGT 261
 QY 241 FOKWAAVVPVSGEEOQRYTCHVQHEGLPOPLILRW 274
 DB 262 FOKWAAVVPVSGEEOQRYTCHVQHEGLPOPLILRW 295
 RESULT 5
 AAH62991 PRELIMINARY; PRT; 346 AA.
 AC AAH62991;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE HLA-F protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC062991; AAH62991.1; -
 SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;
 Query Match 100.0%; Score 274; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.5e-280;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
 DB 22 GSHSLRYSTAVSRPGSGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81

QY 61 EMTTCYAKAQAQTDVRLNLLRYNSOESAGSHLTQMGNGDMGPDGRLIRGYHGHAYDG 120
 DB 82 EMTTCYAKAQAQTDVRLNLLRYNSOESAGSHLTQMGNGDMGPDGRLIRGYHGHAYDG 141
 QY 121 KYDISLNEDLRSWTAADTAQITQRFYEAEBEFTYLEGCELELLRRYLENGKETLQ 180
 DB 142 KYDISLNEDLRSWTAADTAQITQRFYEAEBEFTYLEGCELELLRRYLENGKETLQ 201
 QY 181 RADPKKAVHHPSTSDHEATRLCWALGFYDAEITLTWQDGEOTDSELVETRAGDGT 240
 DB 202 RADPKKAVHHPSTSDHEATRLCWALGFYDAEITLTWQDGEOTDSELVETRAGDGT 261
 QY 241 FQKWAUVVPSGEBQRYTCHVQHEGLFQPLILRW 274
 DB 262 FQKWAUVVPSGEBQRYTCHVQHEGLFQPLILRW 295

RESULT 6

HLAF HUMAN STANDARD; PRT; 362 AA.
 AC P30511; Q3TP68;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDAL2).
 GN Name=HLA-F; Synonyms=HLAF, HLA-5.4;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90111605; PubMed=1689605;
 RA Geraghty D.E., Wei X., Ori H.T., Koller B.H.;
 RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element.";
 RT J. Exp. Med. 171:1-18(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91197889; PubMed=1707659;
 RA Luty D., Epstein H., Holmes N.;
 RT "The human class I MHC gene HLA-F is expressed in lymphocytes.";
 RT Int. Immunol. 2:531-537(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20189617; PubMed=10727083;
 RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcellet M.,
 RA Motier S., Dreano S., Gaius M.T., Hirt C., Soriano N., Galibert F.;
 RT "A 356-Kb sequence of the subtelomeric part of the MHC class I region.";
 RT DNA Seq. 10:263-299(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20189617; PubMed=10727083;
 RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcellet M.,
 RA Motier S., Dreano S., Gaius M.T., Hirt C., Soriano N., Galibert F.;
 RT "A 356-Kb sequence of the subtelomeric part of the MHC class I region.";
 RT DNA Seq. 10:263-299(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Mungall A.J., Palmer M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.P.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S., Clark S., Clegg S., Clegg V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Cullley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,

RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 RA Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
 RA Hamble S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLeay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Seale S.M.,
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L., Wray P.W.,
 RA Whittaker H., Wild A., Willey D.J., Wilmer F.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811(2003).
 CC -1- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
 CC -1- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
 CC
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 CC
 CC EMBL; X17093; CAA34947.1; -;
 CC EMBL; AF055066; AAC34827.1; -;
 CC EMBL; AF000521; BAB63337.1; -;
 CC EMBL; AL022723; CAB46623.1; -;
 CC PIR; A60384; A60384.
 CC HSSP; Q29961; LHSN.
 CC Genew; HGNC:4963; HLA-F.
 CC MIM; 143110; -;
 CC GO; GO:0030106; F:MHC class I receptor activity; TAS.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_c1.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR001039; MHC I.
 CC InterPro; IPR010579; MHC_I_C.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC Pfam; PF06623; MHC_I_C; 1.
 CC PRINTS; PR01639; MHCCLASSI.
 CC ProDom; PD000050; MHC I; 1.
 CC SMART; SM00407; Ig_c1; 1.
 CC PROSITE; PS00835; IG LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC GlycoProtex; MHC I; Polymorphism; Signal; Transmembrane.
 CC SIGNAL; 1 21
 CC CHAIN; 22 362
 CC
 CC HLA class I histocompatibility antigen, alpha chain F.
 CC Extracellular alpha-1.
 CC Extracellular alpha-2.
 CC Extracellular alpha-3.
 CC Connecting peptide.
 CC Cytoplasmic tail.
 CC By similarity.
 CC Similarity.
 CC N-linked (GlcNAc...) (By similarity).
 CC S -> P (in dbSNP:1736924).
 CC VARIANT; 272

FT SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64; /FTID=VAR 018327.

Query Match 100.0%; Score 274; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 22 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81

QY 61 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGVHQAHDG 120
DB 82 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGVHQAHDG 141

QY 121 KYIISINEDLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRYLNGKETLQ 180
DB 142 KYIISINEDLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRYLNGKETLQ 201

QY 181 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 240
DB 202 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 261

QY 241 FOKWAAVVPSEEGRYTCHVQHEGLPOPLILRW 274
DB 262 FOKWAAVVPSEEGRYTCHVQHEGLPOPLILRW 295

RESULT 7
BAC54915
ID BAC54915 PRELIMINARY; PRT; 362 AA.
AC BAC54915
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DE Major histocompatibility complex, class I, F.
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT "Genome diversity in HLA: A new strategy for detection of genetic
RT polymorphisms in expressed genes within the HLA class III and class I
RT regions";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086082; BAC54915.1; --
SQ SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;

Query Match 100.0%; Score 274; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 22 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 81

QY 61 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGVHQAHDG 120
DB 82 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGVHQAHDG 141

QY 121 KYIISINEDLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRYLNGKETLQ 180
DB 142 KYIISINEDLRSWTAADTVAQITQRFYAEAYAEFFRYLGECELELLRYLNGKETLQ 201

QY 181 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 240
DB 202 RADPPKHAHVHPIISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVEVTRPAGDGT 261

QY 241 FOKWAAVVPSEEGRYTCHVQHEGLPOPLILRW 274

DB 262 FOKWAAVVPSEEGRYTCHVQHEGLPOPLILRW 295

RESULT 8
Q95HCO
ID Q95HCO PRELIMINARY; PRT; 460 AA.
AC Q95HCO
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE HLA-F protein (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009260; AAH09260.2; --
DR HSSP; Q29961; IHSB.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00129; MHC_L; 1.
DR PRINTS; PR01838; MHCCLASS1.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER
SQ SEQUENCE 460 AA; 52263 MW; CIA0B6891978D93E CRC64;

Query Match 100.0%; Score 274; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 4.6e-280;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 60
DB 40 GSHSLRYFTAVSRGRGEPRIYAVYDDTQFLRFDSDAAIPRMEPRFPWVEQGPQYW 99

QY 61 EMTTGAKANAQTDVALNLLRRYNQSEAGSHTLQGMNGCDMGDPDGLLRGVHQAHDG 120

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Db 100 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQNMNGCDMGPDPGRLLRGYHAYDVG 159
Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRRYLENGKETLQ 180
Db 160 KDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRRYLENGKETLQ 219
Qy 181 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 220 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 279
Qy 241 FQKWAAVVVP 250
Db 262 FQKWAAVVVP 271

RESULT 9
QBMGQ1
ID QBMGQ1 PRELIMINARY; PRT; 346 AA.
AC QBMGQ1;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF523284; AA74979.1; -
DR EMBL; AF523291; AA74986.1; -
DR EMBL; AF523292; AA74987.1; -
DR EMBL; AY645748; AA73231.1; -
DR EMBL; AY645754; AA73237.1; -
DR HSSP; Q29961; 1HSA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_VHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PR01638; MECCASSI.
DR PRODOM; PD000050; MHC I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_VHC; 1.
KW Transmembrane.
SQ SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;

Query Match 91.2%; Score 250; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.8e-255;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSHSLRFSFSTAVSRPGSGERYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQSGPYW 60
Db 22 GSHSLRFSFSTAVSRPGSGERYIAVEYVDDTQFLRFDSDAAIPRMEPREPWEQSGPYW 81

Qy 61 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQNMNGCDMGPDPGRLLRGYHAYDVG 120
Db 82 EWTGYAKANAQTRVALRNLRRYNQSEAGSHTLQNMNGCDMGPDPGRLLRGYHAYDVG 141

Qy 121 KDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRRYLENGKETLQ 180
Db 142 KDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRRYLENGKETLQ 201

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Qy 181 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 240
Db 202 RADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDELVEVTRPAGDGT 261
Qy 241 FQKWAAVVVP 250
Db 262 FQKWAAVVVP 271

RESULT 10
Q6DU20
ID Q6DU20 PRELIMINARY; PRT; 346 AA.
AC Q6DU20;
DT 01-OCT-2004 (TREMELrel. 28, Created)
DT 01-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMELrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY645755; AA773238.1; -
SQ SEQUENCE 346 AA; 39082 MW; 6F739AA41917E7B2 CRC64;

Query Match 81.8%; Score 224; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.2e-227;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 WVEQGPQYEWTTGYAKANAQTRVALRNLRRYNQSEAGSHTLQNMNGCDMGPDPGRLL 110
Db 72 WVEQGPQYEWTTGYAKANAQTRVALRNLRRYNQSEAGSHTLQNMNGCDMGPDPGRLL 131
Qy 111 RGYHGHAYDGDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRR 170
Db 132 RGYHGHAYDGDYISLNEDLSRWTAADTVAQITQRFYEAEAEAEFRTYLEGECELELLRR 191
Qy 171 YLENGKETLQRADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDEL 230
Db 192 YLENGKETLQRADPPKHAHVHPISDHEATLRCAWLGFGYPAEITLTWQDGEQOTDEL 251
Qy 231 VETRPAGDGTFOKWAAVVVP 274
Db 252 VETRPAGDGTFOKWAAVVVP 295

RESULT 11
Q95IT2
ID Q95IT2 PRELIMINARY; PRT; 346 AA.
AC Q95IT2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE MHC class I antigen.
GN Name=Patr-F;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21291697; PubMed=11398964;
RA Adams E.J., Parham P.;
RT "Genomic analysis of common chimpanzee major histocompatibility
complex class I genes.";
RL Immunogenetics 53:200-208(2001).
DR EMBL; AF338355; AAK77479.1; -
DR HSSP; Q29961; 1HSA.

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GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF07654; Cl-set; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS0835; IG LIKE; 1.
 DR PROSITE: PS0290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;
 SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;
 Query Match 75.9%; Score 208; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.7e-210;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 122
 DB 84 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 143
 QY 123 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 182
 DB 144 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 203
 QY 183 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 242
 DB 204 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 263
 QY 243 KWAANVVPSEGEQRYTCHVQHEGLPOPL 270
 DB 264 KWAANVVPSEGEQRYTCHVQHEGLPOPL 291
 RESULT 12
 QYR27 PRELIMINARY; PRT; 362 AA.
 ID QYR27 PRELIMINARY; PRT; 362 AA.
 AC QYR27; 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Class IB.
 GN Name=Patr-F;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22709134; PubMed=12799463;
 RA Anzai T., Shina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
 RA Yamagata T., Kulsiki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
 RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
 RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
 RT "Comparative sequencing of human and chimpanzee MHC class I regions
 RT unveils insertions/deletions as the major path to genomic
 RT divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
 RL EMBL: AB100087; BAC718191.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF07654; Cl-set; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS0835; IG LIKE; 1.
 DR PROSITE: PS0290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;
 SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;
 Query Match 75.9%; Score 208; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.7e-210;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 122
 DB 84 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 143
 QY 123 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 182
 DB 144 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 203
 QY 183 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 242
 DB 204 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 263
 QY 243 KWAANVVPSEGEQRYTCHVQHEGLPOPL 270
 DB 264 KWAANVVPSEGEQRYTCHVQHEGLPOPL 291
 RESULT 12
 QYR27 PRELIMINARY; PRT; 362 AA.
 ID QYR27 PRELIMINARY; PRT; 362 AA.
 AC QYR27; 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Class IB.
 GN Name=Patr-F;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22709134; PubMed=12799463;
 RA Anzai T., Shina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
 RA Yamagata T., Kulsiki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
 RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
 RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
 RT "Comparative sequencing of human and chimpanzee MHC class I regions
 RT unveils insertions/deletions as the major path to genomic
 RT divergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
 RL EMBL: AB100087; BAC718191.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF07654; Cl-set; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS0835; IG LIKE; 1.
 DR PROSITE: PS0290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;
 SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;
 Query Match 75.9%; Score 208; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.8e-210;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 122
 DB 84 TTGYAKANAQTDRLVALRNLRLRYNQSEAGSHTLQGMNGCDMPGDRLLRGVGHAYDGKD 143
 QY 123 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 182
 DB 144 YISLNEDLSWTAADTAQITQRFYEAEYAEAEPTYLEGECLELLRYLNGKETLQRA 203
 QY 183 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 242
 DB 204 DPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEQQTDTLQVETRPAGDGTQ 263
 QY 243 KWAANVVPSEGEQRYTCHVQHEGLPOPL 270
 DB 264 KWAANVVPSEGEQRYTCHVQHEGLPOPL 291
 RESULT 13
 Q860R0 PRELIMINARY; PRT; 254 AA.
 ID Q860R0 PRELIMINARY; PRT; 254 AA.
 AC Q860R0; 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE MHC class Ib antigen.
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Liu Y., He X., Xu L., Zeng Y.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY253271; AAC86775.1; -.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SEQUENCE 254 AA; 28568 MW; C81F225DA09AAED2 CRC64;
 Query Match 66.4%; Score 182; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 3.7e-183;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSHSLRYFSTAVSPRGGEPR

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:13:46 : Search time 28.0164 Seconds
(without alignments)
941.000 Million cell updates/sec

Title: US-09-819-371-5

Perfect score: 274

Sequence: 1 GSHSLRFSTAVSRPGRGEP.....QRYTCHVQHGLPQLRLW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	274	100.0	362	2 AG0384	MHC class I histoc
2	126	46.0	345	2 S07114	MHC class I histoc
3	73	26.6	316	2 C37028	MHC class I histoc
4	59	21.5	348	2 S29990	histocompatibility
5	44	16.1	275	1 HLU10	MHC class I histoc
6	44	16.1	298	2 S4994	class I histocompa
7	44	16.1	313	2 I36958	MHC class I histoc
8	44	16.1	325	2 I54449	MHC class I HLA-Cx
9	44	16.1	332	2 S06424	MHC class I histoc
10	44	16.1	345	2 I68749	MHC class I lympho
11	44	16.1	354	2 I54551	histocompatibility
12	44	16.1	357	2 I36966	MHC class I protei
13	44	16.1	357	2 I36965	MHC class I protei
14	44	16.1	359	1 HLU12	MHC class I histoc
15	44	16.1	364	2 S03535	class I histocompa
16	44	16.1	365	2 S01171	MHC class I histoc
17	44	16.1	365	2 I36961	MHC class I histoc
18	44	16.1	365	2 I37476	MHC class I histoc
19	44	16.1	365	2 A47636	MHC class I histoc
20	44	16.1	365	2 I83063	Al1.2 human
21	44	16.1	365	2 I36039	HLA-A30.3 precurs
22	44	16.1	365	2 I61856	MHC class I histoc
23	44	16.1	365	2 I37478	MHC class I histoc
24	44	16.1	365	2 I54493	MHC class I histoc
25	44	16.1	365	2 S77963	MHC class I histoc
26	44	16.1	365	2 I38519	MHC class I histoc
27	44	16.1	365	2 I54416	HLA-AW24 protein -
28	44	16.1	365	2 I38518	HLA-A-0102 allele
29	44	16.1	366	1 HLUW3	MHC class I histoc

ALIGNMENTS

RESULT 1

AG0384

MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C:Species: Homo sapiens (man)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004

C:Accession: AG0384; J0147

Ribury, D.; Epstein, H.; Holmes, N.

Int. Immunol. 2, 531-537, 1990

A:Title: The human class I MHC gene HLA-F is expressed in lymphocytes.

A:Reference number: AG0384; MUID:91197689; PMID:1707659

A:Accession: AG0384

A:Molecule type: DNA

A:Residues: 1-362 <LUR>

A:Cross-references: UNIPROT:P30511

R:Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.

J. Exp. Med. 171, 1-18, 1990

A:Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I

A:Reference number: J0147; MUID:90111605; PMID:1688605

A:Accession: J0147

A:Molecule type: DNA

A:Residues: 1-362 <GER>

A:Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407

A:Experimental source: lymphoblastoid cell line

C:Genetics:

A:Gene: GDB:HLA-F

A:Cross-references: GDB:125714

A:Map position: 6p21.3-6p21.3

A:Introns: 22/1, 12/1, 204/1, 296/1, 335/1, 346/1, 362/1

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: Glycoprotein; heterodimer; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-111/Domain: alpha-1 <AL1>

F:78-104/Region: hypervariable

F:112-203/Domain: alpha-2 <AL2>

F:164-192/Region: hypervariable

F:204-295/Domain: alpha-3 <AL3>

F:217-282/Domain: immunoglobulin homology <IMM>

F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 274; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 1.1e-282;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRFSTAVSRPGRGEPRIYAVEYVDTQFLRFDSDAAIPRMPEPRFWVEQGPQW 60

DB 22 GSHSLRFSTAVSRPGRGEPRIYAVEYVDTQFLRFDSDAAIPRMPEPRFWVEQGPQW 81

QY 61 EWTGYAKAQAQTDRLVALNLLRRYNOSEAGSTLQMGNCMDGPDGRLLRGHQYAYDG 120

DB 82 EWTGYAKAQAQTDRLVALNLLRRYNOSEAGSTLQMGNCMDGPDGRLLRGHQYAYDG 141

QY 121 KDYISLNEDLSKTSWTAADTVAQITQRFYEABEYAEFFYLEGECLELLRLRYLENGKETLQ 180

MHC class I histoc

class I histocompa

lymphocyte antigen

MHC class I histoc

MHC class I histoc

lymphocyte antigen

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Db 142 KDYSLNEDLRSWTAADTVAQITQRFYAEAEAEFFTYLEGECELELLRRYLENGKETLQ 201
 Qy 181 RADPPKARVAHPISDHEATLRCWALGFYPABITLWQDGEQOTDELVEVTRPAGDGT 240
 Db 202 RADPPKARVAHPISDHEATLRCWALGFYPABITLWQDGEQOTDELVEVTRPAGDGT 261
 Qy 241 FQKWAAVVPSGGEORVYCHVQHEGLPPLIRW 274
 Db 262 FQKWAAVVPSGGEORVYCHVQHEGLPPLIRW 295

RESULT 2

S07114
 MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S07114
 R:Lawlor, D.A.; Ward, P.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
 Nature 335, 268-271, 1988
 A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
 A:Reference number: S06424; MUID:88319000; PMID:3412487
 A:Accession: S07114
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-345 <LAW>
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: glycoprotein; membrane protein
 F:217-282/Domain: immunoglobulin homology <IMM>

Query Match 46.0%; Score 126; DB 2; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.7e-125; Mismatches 0; Indels 0; Gaps 0;

Qy 63 TTGAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGD 122
 Db 84 TTGAKANAQTDRLVALNLLRRYNSQAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGD 143
 Qy 123 YISLNEDLRSWTAADTVAQITQRFYAEAEAEFFTYLEGECELELLRRYLENGKETLORA 182
 Db 144 YISLNEDLRSWTAADTVAQITQRFYAEAEAEFFTYLEGECELELLRRYLENGKETLORA 203

RESULT 3

C37028
 MHC class I histocompatibility antigen HLA-C (clone 9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 14-Feb-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
 C:Accession: C37028
 R:Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella
 Immunogenetics 29, 80-91, 1989
 A:Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of
 A:Reference number: A37028; MUID:8912144; PMID:2514713
 A:Accession: C37028
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-316 <CIA>
 A:Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q29987; UNIPROT:Q9MY34; UNIPROT:O19677; UNIP
 C:Genetics:
 A:Gene: GDB:HLA-C
 A:Cross-references: GDB:119311; OMIM:142840
 A:Map position: 6p21.3-6p21.3
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F:170-235/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 73; DB 2; Length 316;

Best Local Similarity 100.0%; Pred. No. 3e-69; Mismatches 0; Indels 0; Gaps 0;

Qy 195 SDEATLRCWALGFYPABITLWQDGEQOTDELVEVTRPAGDGTQKWAAVVPSGEE 254
 Db 169 SDEATLRCWALGFYPABITLWQDGEQOTDELVEVTRPAGDGTQKWAAVVPSGEE 228
 Qy 255 QRYTCHVQHEGLP 267
 Db 229 QRYTCHVQHEGLP 241

RESULT 4

S29990
 histocompatibility antigen, HLA-F-like - rhesus macaque
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S29990
 R:Bontrop, R.R.
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S29990
 A:Accession: S29990
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-348 <BON>
 A:Cross-references: UNIPROT:P33617; EMBL:Z21819; NID:G38568; PIDN:CAA79885.1; PID:G38569
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:219-284/Domain: immunoglobulin homology <IMM>

Query Match 21.5%; Score 59; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 2.5e-54; Mismatches 0; Indels 0; Gaps 0;

Qy 212 EITLWQDGEQOTDELVEVTRPAGDGTQKWAAVVPSGGEORVYCHVQHEGLP 270
 Db 235 EITLWQDGEQOTDELVEVTRPAGDGTQKWAAVVPSGGEORVYCHVQHEGLP 293

RESULT 5

HLH10
 MHC class I histocompatibility antigen HLA-A10 alpha chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: B24512
 R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
 J. Biol. Chem. 260, 13414-13423, 1985
 A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc

A:Reference number: A92500; MUID:86033791; PMID:3863816

A:Accession: B24512

A:Molecule type: DNA

A:Residues: 1-275 <DAV>

A:Cross-references: UNIPROT:P01892; GB:M11887; NID:G184157; PIDN:AAA52656.1; PID:G184158

C:Genetics:

A:Gene: GDB:HLA-A

A:Cross-references: GDB:119310; OMIM:142800

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

F:130-195/Domain: immunoglobulin homology <IMM>

F:130-195/Domain: immunoglobulin homology (Asn) (covalent) #status predicted

Query Match 16.1%; Score 44; DB 1; Length 275;

Best Local Similarity 100.0%; Pred. No. 1.7e-38;

Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQDELVEVTRPAGDGTQKWAAVVPSGGEORVYCHVQHEGLP 267

Db 158 QTQDELVEVTRPAGDGTQKWAAVVPSGGEORVYCHVQHEGLP 201

RESULT 6

S44994

class I histocompatibility antigen HLA-Cw6 precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C/Accession: S44994
 R/Marget, M.; Brockstedt, D.; Jenisch, S.
 submitted to the EMBL Data Library, May 1994
 A/Description: New HLA-Cw6 sequence.
 A/Reference number: S44994
 A/Accession: S44994
 A/Molecule type: mRNA
 A/Residues: 1-298 <VAR>
 A/Cross-references: UNIPROT:Q29866; EMBL:Z33459; NID:G488361; PID:G488361
 C/Species: Pan troglodytes (chimpanzee)
 F:1-72/Domain: class I histocompatibility antigen; immunoglobulin homology
 F:73-298/Product: class I histocompatibility antigen HLA-Cw6 (fragment) #status predicted
 F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267
 DB 248 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 291

RESULT 7
 MHC class I chain - chimpanzee (fragment)
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 02-Jul-1995 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I36958
 R/Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
 J. Immunol. 142, 3937-3950, 1989
 A/Title: Diversity and diversification of HLA-A,B,C alleles.
 A/Reference number: I36956; MUID:89235215; PMID:2715640
 A/Accession: I36958
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-333 <RES>
 A/Cross-references: UNIPROT:Q30989; GB:M24046; NID:G176816; PID:G176817
 C/Species: class I histocompatibility antigen; immunoglobulin homology
 F:167-232/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267
 DB 195 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 238

RESULT 8
 MHC class I HLA-Cx52 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jan-2000
 C/Accession: I54449
 R/Takata, H.; Inoko, H.; Ando, A.; Haranaka, M.; Watanabe, B.; Tsuji, K.; Iri, H.
 Immunogenetics 28, 265-270, 1988
 A/Title: Cloning and analysis of HLA class I cDNA encoding a new HLA-C specificity Cx52.
 A/Reference number: I54449; MUID:89330144; PMID:2843461
 A/Accession: I54449
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-325 <RES>
 A/Cross-references: GB:M21963; NID:G188540; PID:AAA59847.1; PID:G188541
 C/Genetics:
 A/Gene: GDB:HLA-C
 A/Cross-references: GDB:119311; OMIM:142840
 A/Map position: gp1.3-gp2.3
 C/Species: class I histocompatibility antigen; immunoglobulin homology
 F:179-244/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 325;

Best Local Similarity 100.0%; Pred. No. 2e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267
 DB 207 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 250

RESULT 9
 MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee
 N/Alternate names: MHC Ch1a chain
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S06424; I36959
 R/Lawlor, D.A.; Ward, F.B.; Ennis, P.D.; Jackson, A.P.; Parham, P.
 Nature 335, 268-271, 1988
 A/Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
 A/Reference number: S06424; MUID:89319000; PMID:3412487
 A/Accession: S06424
 A/Molecule type: mRNA
 A/Residues: 1-332 <LAW>
 A/Cross-references: UNIPROT:Q30990
 R/Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
 J. Immunol. 142, 3937-3950, 1989
 A/Title: Diversity and diversification of HLA-A,B,C alleles.
 A/Reference number: I36956; MUID:89235215; PMID:2715640
 A/Accession: I36959
 A/Molecule type: mRNA
 A/Residues: 1-332 <RES>
 A/Cross-references: GB:M24047; NID:G176818; PID:AAA5426.1; PID:G553155
 C/Species: class I histocompatibility antigen; immunoglobulin homology
 C/Keywords: glycoprotein; membrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-114/Domain: alpha-1 #status predicted <EX1>
 F:115-206/Domain: alpha-2 #status predicted <EX2>
 F:220-285/Domain: immunoglobulin homology <IMM>
 F:307-331/Domain: transmembrane #status predicted <TM>
 F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:125-188,227-283/Disulfide bonds: #status predicted

Query Match 16.1%; Score 44; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267
 DB 248 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 291

RESULT 10
 MHC class I lymphocyte antigen - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C/Accession: I68749
 R/Pohl, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
 Immunogenetics 29, 297-307, 1989
 A/Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B a
 A/Reference number: I54457; MUID:89233295; PMID:2714852
 A/Accession: I68749
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-345 <RES>
 A/Cross-references: UNIPROT:Q29963; GB:M28206; NID:G576476; PID:AAA57258.1; PID:G576477
 C/Species: class I histocompatibility antigen; immunoglobulin homology
 F:199-264/Domain: immunoglobulin homology <IMM>

Query Match 16.1%; Score 44; DB 2; Length 345;
 Best Local Similarity 100.0%; Pred. No. 2.1e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTGFKWAAVVPVSGEQRVYCHVQHEGLP 267

F;219-284/Domain: immunoglobulin homology <IMM>
 F;298-336/Domain: transmembrane #status predicted <TM>
 F;337-364/Domain: intracellular #status predicted <INT>

Query Match 16.1%; Score 44; DB 2; Length 364;
 Best Local Similarity 100.0%; Pred. No. 2.2e-38;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRYTCHVQHEGLP 267
 |||||
 Db 247 QTQDTLVETRPAGDGTQKWAADVVPSSGEQRYTCHVQHEGLP 290
 |||||

Search completed: December 15, 2004, 18:25:17
 Job time : 29.0164 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:14:01 ; Search time 30.818 Seconds
(without alignments)
589.627 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRYFSTAVSRGGRGP.....QRYTCHVQHGGLPQPLILRW 274

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/6C COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	99	36.1	120	4	US-09-513-999C-4290	Sequence 4290, App
2	44	15.1	274	1	US-08-222-851-1	Sequence 1, Appl
3	39	14.2	117	2	US-08-486-057-9	Sequence 9, Appl
4	39	14.2	117	3	US-08-958-316-9	Sequence 9, Appl
5	39	14.2	145	2	US-08-406-057-8	Sequence 8, Appl
6	39	14.2	145	3	US-08-958-316-8	Sequence 8, Appl
7	30	10.9	289	2	US-08-484-905-79	Sequence 79, Appl
8	30	10.9	289	3	US-08-481-985B-79	Sequence 79, Appl
9	30	10.9	289	3	US-08-370-476-79	Sequence 79, Appl
10	29	10.6	274	2	US-08-484-905-105	Sequence 105, App
11	29	10.6	274	2	US-08-484-905-107	Sequence 107, App
12	29	10.6	274	2	US-08-484-905-108	Sequence 108, App
13	29	10.6	274	3	US-08-481-985B-105	Sequence 105, App
14	29	10.6	274	3	US-08-481-985B-107	Sequence 107, App
15	29	10.6	274	3	US-08-481-985B-108	Sequence 108, App
16	29	10.6	274	3	US-08-370-476-105	Sequence 105, App
17	29	10.6	274	3	US-08-370-476-107	Sequence 107, App
18	29	10.6	274	3	US-08-370-476-108	Sequence 108, App
19	29	10.6	341	3	US-08-890-719-38	Sequence 38, App
20	29	10.6	365	2	US-08-484-905-97	Sequence 97, Appl
21	29	10.6	365	2	US-08-484-905-98	Sequence 98, Appl
22	29	10.6	365	2	US-08-484-905-99	Sequence 99, Appl
23	29	10.6	365	2	US-08-484-905-100	Sequence 100, App
24	29	10.6	365	2	US-08-484-905-101	Sequence 101, App
25	29	10.6	365	2	US-08-481-985B-97	Sequence 97, Appl
26	29	10.6	365	3	US-08-481-985B-98	Sequence 98, Appl
27	29	10.6	365	3	US-08-481-985B-99	Sequence 99, Appl

28 29 10.6 365 3 US-08-481-985B-100 Sequence 100, App
29 29 10.6 365 3 US-08-481-985B-101 Sequence 101, App
30 29 10.6 365 3 US-08-652-265-23 Sequence 23, Appl
31 29 10.6 365 3 US-08-834-497A-23 Sequence 23, Appl
32 29 10.6 365 3 US-08-370-476-97 Sequence 97, Appl
33 29 10.6 365 3 US-08-370-476-98 Sequence 98, Appl
34 29 10.6 365 3 US-08-370-476-99 Sequence 99, Appl
35 29 10.6 365 3 US-08-370-476-100 Sequence 100, App
36 29 10.6 365 3 US-08-370-476-101 Sequence 101, App
37 29 10.6 365 3 US-09-503-444A-23 Sequence 23, Appl
38 27 9.9 184 2 US-08-484-905-83 Sequence 83, Appl
39 27 9.9 184 3 US-08-481-985B-83 Sequence 83, Appl
40 27 9.9 184 3 US-08-370-476-83 Sequence 83, Appl
41 25 9.1 108 2 US-08-484-905-82 Sequence 82, Appl
42 25 9.1 108 3 US-08-481-985B-82 Sequence 82, Appl
43 25 9.1 108 3 US-08-370-476-82 Sequence 82, Appl
44 25 9.1 290 2 US-08-484-905-80 Sequence 80, Appl
45 25 9.1 290 3 US-08-481-985B-80 Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLLLLSGALALT/DT

US-09-513-999C-4290

Query Match 36.1%; Score 99; DB 4; Length 120;

Best Local Similarity 100.0%; Pred. No. 28-90;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSTAVSRGGRGPYAVYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQY 60

Db 22 GSHSLRYFSTAVSRGGRGPYAVYVDDTQFLRFDSDAAIPRMEPRPWEQEGPQY 81

QY 61 EWTGAKANAQTDVVALNLLRRYVQSEAGSHLQGMN 99

Db 82 EWTGAKANAQTDVVALNLLRRYVQSEAGSHLQGMN 120

RESULT 2

US-08-222-851-1

; Sequence 1, Application US/08222851

; Patent No. 5723128

; GENERAL INFORMATION:

; APPLICANT: CLAYBERGER, CAROL A.

; APPLICANT: KRENSKY, ALAN M.

; APPLICANT: PARHAM, PETER

; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")

```

; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQTELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 267
DB 224 QTQTELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 267

RESULT 3
US-08-406-057-9
; Sequence 9, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,057
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179

; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-222-851-1

Query Match 16.1%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQTELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 267
DB 224 QTQTELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 267

RESULT 3
US-08-406-057-9
; Sequence 9, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,057
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
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```

; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-331-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-057-9

Query Match 14.2%; Score 39; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 267
DB 51 ELVETRPAGDGTFOKWAAVVPSGEQRYTCHVOHGLP 89

RESULT 4
US-08-958-316-9
; Sequence 9, Application US/08958316
; Patent No. 6231659
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,316
; FILING DATE: 27-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0846-0437-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-958-316-9

Query Match 14.2%; Score 39; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267
Db 51 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 89

RESULT 5

US-08-406-057-8
; Sequence 8, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406.057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 7.6e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267
Db 79 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 117

RESULT 6

US-08-958-316-8
; Sequence 8, Application US/08958316
; Patent No. 6291659
; GENERAL INFORMATION:

APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958.316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-0437-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-958-316-8

Query Match 14.2%; Score 39; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 7.6e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 267
Db 79 ELVETRPAGDGTFOKWAHVVPVSGEQRVYCHVQHEGLP 117

RESULT 7

US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:

APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTFRPAGDGTFOKWAHVVPSSGEQ 255
DB 226 QDTELVTFRPAGDGTFOKWAHVVPSSGEQ 255

RESULT 8
US-08-481-985B-79
Sequence 79, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-79

Query Match 10.9%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 QDTELVTFRPAGDGTFOKWAHVVPSSGEQ 255
DB 226 QDTELVTFRPAGDGTFOKWAHVVPSSGEQ 255

RESULT 9
US-08-370-476-79
Sequence 79, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lene, Yu-Chun
APPLICANT: Ocius, David
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 79;
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-79

Query Match 10.6%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 QTELVETRPAGDGTQKWAAVVPSGSEQ 255
Db 226 QTELVETRPAGDGTQKWAAVVPSGSEQ 255

RESULT 10

US-08-484-905-105
Sequence 105, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:

APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
Complex (MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS: 127
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner

STREET: 1300 I Street, N.W., Suite 700
CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS-/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,905

FILING DATE: 07-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-105

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQTELVETRPAGDGTQKWAAVVPSG 252

Db 224 QTQTELVETRPAGDGTQKWAAVVPSG 252

RESULT 11

US-08-484-905-107

Sequence 107, Application US/08484905

Patent No. 5976551

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: An Altered Major Histocompatibility

Complex (MHC) Determinant and Methods for Using the

TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS-/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,905

FILING DATE: 07-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 03495.0106-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 274 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-107

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 QTQTELVETRPAGDGTQKWAAVVPSG 252

Db 224 QTQTELVETRPAGDGTQKWAAVVPSG 252

RESULT 12

US-08-484-905-108

Sequence 108, Application US/08484905

Patent No. 5976551

GENERAL INFORMATION:

APPLICANT: Mottez, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

TITLE OF INVENTION: An Altered Major Histocompatibility

NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03495.0106-04000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 107:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 274 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-481-985B-107

Query Match 10.6%; Score 29; DB 3; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252

RESULT 15

US-08-481-985B-108
 ; Sequence 108, Application US/08481985B
 ; Patent No. 6011146
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; TITLE OF INVENTION: Altered Major Histocompatibility Complex
 ; NUMBER OF SEQUENCES: 148
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 ; ADDRESSES: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/481.985B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 03495.0106-04000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 108:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 274 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-481-985B-108

Query Match 10.6%; Score 29; DB 3; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252
 DB 224 QTQDTLVETRPAGDGTQKWAAVVPSG 252
 Search completed: December 15, 2004, 18:26:18
 Job time : 31.818 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:02:13 ; Search time 5019 Seconds
(without alignments)
10260.706 Million cell updates

Title: US-09-819-371-1
Perfect score: 1089
Sequence: 1 atggcgcccggaagcctct.....tcacagctataaaagtgtga 1089

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1089	100.0	1089	6	BD187421 Cancer pr
3	1089	100.0	1089	6	B63813 Cancer cell
4	1089	100.0	1089	6	AX525255 Sequence
5	1089	100.0	1089	6	CQ776417 Sequence
6	1089	100.0	1188	9	CQ776511 Sequence
7	1037	95.2	1041	9	AX253270 Homo sapi
8	986	90.5	1041	9	AX253269 Homo sapi
9	986	90.5	1167	9	BC082991 Homo sapi
10	927	85.1	1523	9	BC009260 Homo sapi
11	921	84.6	972	9	AX096962 Homo sapi
12	921	84.6	972	9	AY216682 Homo sapi
13	822	75.5	822	6	AY221102 Homo sapi
14	822	75.5	822	6	BD187422 Cancer pr
15	822	75.5	822	6	E63814 Cancer cell
16	689	63.3	1150	6	AX525256 Sequence
17	645	59.2	645	6	CQ722314 Sequence
18	645	59.2	645	6	BD187423 Cancer pr
19	645	59.2	645	6	E63815 Cancer cell
20	645	59.2	645	6	AX525257 Sequence

20	611	56.1	765	9	AY53271	Homo sapi
21	474	43.5	2307	6	QB842290	Sequence
22	474	43.5	2307	9	AK125274	Homo sapi
23	365	33.5	1158	9	CHPWCHBAD	
24	361	33.1	424	6	AX884350	Sequence
25	361	33.1	424	6	BD023960	Sequence
26	279	25.6	4316	6	QB08559	Sequence
27	279	25.6	4316	6	AX302563	Sequence
28	279	25.6	4316	6	AX411069	Sequence
29	279	25.6	4316	6	AX795667	Sequence
30	279	25.6	4316	6	AX822118	Sequence
31	279	25.6	4316	6	AX825758	Sequence
32	279	25.6	4316	9	HSHLAP	
33	279	25.6	6530	9	AB080802	Homo sapi
34	279	25.6	6941	9	AY645744	Homo sapi
35	279	25.6	6941	9	AY645749	Homo sapi
36	279	25.6	6956	9	AY645743	Homo sapi
37	279	25.6	6956	9	AY645745	Homo sapi
38	279	25.6	6956	9	AY645756	Homo sapi
39	279	25.6	6967	9	AF523294	Homo sapi
40	279	25.6	6968	9	AY645742	Homo sapi
41	279	25.6	6968	9	AY645747	Homo sapi
42	279	25.6	6968	9	AY645751	Homo sapi
43	279	25.6	6968	9	AY645752	Homo sapi
44	279	25.6	6968	9	AY645755	Homo sapi
45	279	25.6	6969	9	AY645746	Homo sapi

ALIGNMENTS

BD187421	BD187421	1089 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	Cancer prophylactic/treatment agent.				
DEFINITION	BD187421				
ACCESSION	BD187421.1				
VERSION	GI:32997160				
KEYWORDS	JP 2003012544-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1089)				

	Query Match	100.0%	Score 1089	DB 6	Length 1089
	Best Local Similarity	100.0%	Pred. No. 0		
	Matches 1089	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	ATGCGGCCCGCGAAGCCTCCTCTGTGTCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG	60		
QY	61	CGCGGCTCCCACTCCTTTGAGGTATTTTCAGCACCGCTGTGTCGGGGCCCGCGCGGGAG	120		
Db	61	CGCGGCTCCCACTCCTTTGAGGTATTTTCAGCACCGCTGTGTCGGGGCCCGCGCGGGAG	120		


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RESULT 4
CQ776417
LOCUS       CQ776417               1188 bp      DNA          linear      PAT 11-MAR-2004
DEFINITION   Sequence 103 from Patent EP1394274.
ACCESSION    CQ776417
VERSION      CQ776417.1   GI:45379907
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuohara,K.
TITLE        Methods of testing for bronchial asthma or chronic obstructive
              pulmonary disease
JOURNAL      Patent: EP 1394274-A 103 03-MAR-2004;
              Genex Research, Inc. (JP)
FEATURES     location/Qualifiers
              source
              1..1188
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Query Match      100.0%; Score 1089; DB 6; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCCCGAAGCCTCTCTGCTGCTCTCAGGGCCCTGSCCTGACCGATATTGG 60
DB 1 ATGGCGCCCGAAGCCTCTCTGCTGCTCTCAGGGCCCTGSCCTGACCGATATTGG 60

QY 61 GCGGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGCGGGCCCGCGGGAG 120
DB 61 GCGGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGCGGGCCCGCGGGAG 120

QY 121 CCCGCTATCGCGTGGAGTAGACGACGCAATCTCTGCGGTTCACAGCGAC 180
DB 121 CCCGCTATCGCGTGGAGTAGACGACGCAATCTCTGCGGTTCACAGCGAC 180

QY 181 GCGCGATTCCAGAGTAGGACCGCGGAGCCGTGGTGAGCAAGAGGGCGCGAGTAT 240
DB 181 GCGCGATTCCAGAGTAGGACCGCGGAGCCGTGGTGAGCAAGAGGGCGCGAGTAT 240

QY 241 TGGAGTGGACACACAGGTACGCCAAGGCCAAGCCAGACTGACCGAGTGGCCCTGAGG 300
DB 241 TGGAGTGGACACACAGGTACGCCAAGGCCAAGCCAGACTGACCGAGTGGCCCTGAGG 300

QY 301 AACCTGCTCCGCGCTAACACGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
DB 301 AACCTGCTCCGCGCTAACACGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360

QY 361 GGTGCGACATGGGCGCCGACGAGCGCTCTCTCGGGGTATCACCAGCACCGTACGAC 420
DB 361 GGTGCGACATGGGCGCCGACGAGCGCTCTCTCGGGGTATCACCAGCACCGTACGAC 420

QY 421 GGCAGAGTATCATCTCTCTGAAAGAGAGCCTGCGCTCTGAGACCGCGGACCGGTG 480
DB 421 GGCAGAGTATCATCTCTCTGAAAGAGAGCCTGCGCTCTGAGACCGCGGACCGGTG 480

QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTAC 540
DB 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTAC 540

QY 541 CTGGAGGGGAGTGCTGGAGTTCCTCGGAGATACCTTGGAGATGGAGAGCGGTA 600
DB 541 CTGGAGGGGAGTGCTGGAGTTCCTCGGAGATACCTTGGAGATGGAGAGCGGTA 600

QY 601 CAGCGCGAGATCTCTCAAGAGGACACAGCTTGGCCACCCACCCCTCTCTGACCATGAGGCC 660
DB 601 CAGCGCGAGATCTCTCAAGAGGACACAGCTTGGCCACCCACCCCTCTCTGACCATGAGGCC 660

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QY 661 ACCCTGAGTGTGGGCGCCCTGCTTACCTCGGAGATCAGCTGACCTGGCAGCGG 720
DB 661 ACCCTGAGTGTGGGCGCCCTGCTTACCTCGGAGATCAGCTGACCTGGCAGCGG 720

QY 721 GATGGGAGGAACACAGCCAGGACACAGAGTGTGTGAGACCAAGGCTCGAGGGATGA 780
DB 721 GATGGGAGGAACACAGCCAGGACACAGAGTGTGTGAGACCAAGGCTCGAGGGATGA 780

QY 781 ACCTTCCAGAGTGGGCGCGCTGTGTGCTGCTTCTGAGAGGAACAGAGATACATGC 840
DB 781 ACCTTCCAGAGTGGGCGCGCTGTGTGCTGCTTCTGAGAGGAACAGAGATACATGC 840

QY 841 CATGTGACGACGAGGGGCTGCCCAAGCCCTCATCTGAGATGGGAGGAGTCTCCCGAG 900
DB 841 CATGTGACGACGAGGGGCTGCCCAAGCCCTCATCTGAGATGGGAGGAGTCTCCCGAG 900

QY 901 CCACCATCCCATCTGCGGCATCGTTGCTGGCCCTTCTTCTCTGAGTGTGGTCACT 960
DB 901 CCACCATCCCATCTGCGGCATCGTTGCTGGCCCTTCTTCTCTGAGTGTGGTCACT 960

QY 961 GGAGCTGTGCTGCTGCTGTGATGTGAGGAGAAAGAGCTCAGATAGAAACAGAGGAGC 1020
DB 961 GGAGCTGTGCTGCTGCTGTGATGTGAGGAGAAAGAGCTCAGATAGAAACAGAGGAGC 1020

QY 1021 TACTCTCAGGCTGCAGTCACTGACAGTGGCCAGGGCTCTGGGGTGTCTCTCAGAGTAAT 1080
DB 1021 TACTCTCAGGCTGCAGTCACTGACAGTGGCCAGGGCTCTGGGGTGTCTCTCAGAGTAAT 1080

QY 1081 AAAGTGTA 1089
DB 1081 AAAGTGTA 1089

RESULT 5
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LOCUS       CQ776511               1188 bp      DNA          linear      PAT 11-MAR-2004
DEFINITION   Sequence 197 from Patent EP1394274.
ACCESSION    CQ776511
VERSION      CQ776511.1   GI:45379901
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuohara,K.
TITLE        Methods of testing for bronchial asthma or chronic obstructive
              pulmonary disease
JOURNAL      Patent: EP 1394274-A 197 03-MAR-2004;
              Genex Research, Inc. (JP)
FEATURES     location/Qualifiers
              source
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN

Query Match      100.0%; Score 1089; DB 6; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCCCGAAGCCTCTCTGCTGCTCTCAGGGCCCTGSCCTGACCGATATTGG 60
DB 1 ATGGCGCCCGAAGCCTCTCTGCTGCTCTCAGGGCCCTGSCCTGACCGATATTGG 60

QY 61 GCGGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGCGGGCCCGCGGGAG 120
DB 61 GCGGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGCGGGCCCGCGGGAG 120

QY 121 CCCGCTATCGCGTGGAGTAGACGACGCAATCTCTGCGGTTCACAGCGAC 180
DB 121 CCCGCTATCGCGTGGAGTAGACGACGCAATCTCTGCGGTTCACAGCGAC 180

QY 181 GCGCGATTCCAGAGTAGGACCGCGGAGCCGTGGTGAGCAAGAGGGCGCGAGTAT 240
DB 181 GCGCGATTCCAGAGTAGGACCGCGGAGCCGTGGTGAGCAAGAGGGCGCGAGTAT 240

QY 241 TGGAGTGGACACACAGGTACGCCAAGGCCAAGCCAGACTGACCGAGTGGCCCTGAGG 300
DB 241 TGGAGTGGACACACAGGTACGCCAAGGCCAAGCCAGACTGACCGAGTGGCCCTGAGG 300

QY 301 AACCTGCTCCGCGCTAACACGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360
DB 301 AACCTGCTCCGCGCTAACACGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAAT 360

QY 361 GGTGCGACATGGGCGCCGACGAGCGCTCTCTCGGGGTATCACCAGCACCGTACGAC 420
DB 361 GGTGCGACATGGGCGCCGACGAGCGCTCTCTCGGGGTATCACCAGCACCGTACGAC 420

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DB 421 GGCAGAGTATCATCTCTCTGAAAGAGAGCCTGCGCTCTGAGACCGCGGACCGGTG 480

QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTAC 540
DB 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGGAGTTCAGGACCTAC 540

QY 541 CTGGAGGGGAGTGCTGGAGTTCCTCGGAGATACCTTGGAGATGGAGAGCGGTA 600
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QY 601 CAGCGCGAGATCTCTCAAGAGGACACAGCTTGGCCACCCACCCCTCTCTGACCATGAGGCC 660
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Qy 541 CTGAGGCGAGTGCCTGGAGTTGCTCCGAGATACCTGGAGATGGAGGAGGAGCGCTA 600
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 Db 661 ACCTCAGGTGTGGGCGCTCTACCTCTGGGAGATACAGCTGACCTGCGACGCG 720
 Qy 721 GATGGGAGGAGACAGACCCAGACACAGAGCTGTGGGAGACACAGGCTGTGAGGGGATGGA 780
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 Qy 781 ACCTTCCAGAGTGGGCGCTCTGTGTGGTGGCTCTCTGGAGAGGACACAGATACACATGC 840
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 Qy 841 CATGTGACAGACAGAGGGGTGCGCCAGCCCTCATCTGATGATGGAGAGCTCTCCCGAG 900
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 Qy 961 GGAGCTGT 1020
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 Qy 1021 TACTCTCAGGCTGCGACT 1037
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RESULT 8

BC062991

LOCUS

DEFINITION

Homo sapiens major histocompatibility complex, class I, F, mRNA

(CDNA clone MGC:74962 IMAGE:5496696), complete cds.

ACCSSION

BC062991

VERSION

MGC:74962 IMAGE:5496696

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1167)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, P.,

Diatchenko, I., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Hellon, E., Kettner, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shakhmurov, Y.,

Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

2 (bases 1 to 1167)

Strausberg, R.

Direct Submission

Submitted (01-DEC-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cga@nci.nih.gov

Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@hgr.nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

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Young, A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: INAK Plate: 135 Row: 0 Column: 19

This clone was selected for full length sequencing because it

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REFERENCE
1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Negai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
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AUTHORS   Liu, Y., Xu, L., Zeng, Y. and He, X.
TITLE     A new polymorphism in non-classical MHC class I HLA-F
JOURNAL    Unpublished
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AUTHORS   Liu, Y., Xu, L., Zeng, Y. and He, X.
TITLE     Direct Submission
JOURNAL    Submitted (20-JAN-2003) Key Laboratory of Ministry of Education for
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VERSION
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ORGANISM
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AUTHORS

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BD187422
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JP 2003012544-A/2.
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Egawa,K.

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JOURNAL Patent: JP 2003012544-A 2 15-JAN-2003;
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QY 424 AAGGATTACATCTCCCTGAAACGAGGACCTGCGCTTCCTGGACCGCGCGGACACCGTGGCT 483
DB 361 AAGGATTACATCTCCCTGAAACGAGGACCTGCGCTTCCTGGACCGCGCGGACACCGTGGCT 420
QY 484 CAGATCACCGCGCTTCTATGAGGAGAGGAATATGACAGGAGTTCAGGACTACCTG 543
DB 421 CAGATCACCGCGCTTCTATGAGGAGAGGAATATGACAGGAGTTCAGGACTACCTG 480
QY 544 GAGGCGAGTGGCTGGAGTGTCTCCGAGATATCTTGGAGAAATGGAGAGGAGCGCTACAG 603
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QY 604 CGCGAGATCTCCAAAGGACACGCTTCCCGACCAACCGCCATCTCTGACCATGAGGCGACC 663
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QY 844 GTCCAGCAGAGGGCTGCCAGCCCTCATCTTGATGG 885
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RESULT 14
E63814
LOCUS 822 bp DNA linear PAT 27-AUG-2002
DEFINITION Cancer cell-specific HLA-F antigen and method for diagnosing cancer
using the same.
ACCESSION E63814
VERSION E63814.1 GI:2253652
KEYWORDS JP 2001095584-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 822)
Egawa,K.
Cancer cell-specific HLA-F antigen and method for diagnosing cancer
using the same
Patent: JP 2001095584-A 2 10-APR-2001;
KOJI EGAWA,KK MEDINET,KEIJI KIMURA
OS Homo sapiens (human)
PN JP 2001095584-A/2
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279566
PI KOJI EGAWA
PC C12N15/09,C07K14/82,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/PC
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 124 CGGTACATCGCGTGGAGTACGTACACGACGCAATTCCTCGCGTTCGACAGGAGCC 183
Db 61 CGGTACATCGCGTGGAGTACGTACACGACGCAATTCCTCGCGTTCGACAGGAGCC 120

QY 184 GCGATTCCGAGTGGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCGCGCAGTATTGG 243
Db 121 GCGATTCCGAGTGGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCGCGCAGTATTGG 180

QY 244 GAGTGACACAGGTTAGCCAGGCGCAACGACAGACTGACCGAGTGGCGCTTGAGGAAC 303
Db 181 GAGTGACACAGGTTAGCCAGGCGCAACGACAGACTGACCGAGTGGCGCTTGAGGAAC 240

QY 304 CTGCTCCGCGCTACAAACAGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAATGGC 363
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QY 364 TCGCATGGGCGCGAGCGCTCTCGCGGCTATCACAGACGCGGTACGAGCGC 423
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Db 361 AAGGATTATCTCTCCCTGAAGAGGACCTGGCTCTTGACCGCGGCGGACCGGTGGCT 420
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QY 604 CGCGAGATCTCTCAAAGGCGACAGTTGCCACACCCCATCTCTGACCATGAGGCCACC 663
Db 541 CGCGAGATCTCTCAAAGGCGACAGTTGCCACACCCCATCTCTGACCATGAGGCCACC 600
QY 664 CTGAGGTGCTGGGCGCTTCTACCTCGCGAGATCACGCTGACCTGGGAGCGGGAT 723
Db 601 CTGAGGTGCTGGGCGCTTCTACCTCGCGAGATCACGCTGACCTGGGAGCGGGAT 660
QY 724 GGGAGGACAGACCCAGGACAGAGCTTGTGGAGACAGGCTCTCAGGGATGGAACC 783
Db 661 GGGAGGACAGACCCAGGACAGAGCTTGTGGAGACAGGCTCTCAGGGATGGAACC 720
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Db 721 TTCCAGAGTGGGCGCTGTGCTGTGCTGCTTCTGGAGAGGAAACAGAGATACACATCCCAT 780
QY 844 GTGCAGCAGAGGGGCTGCCCGAGCCCTCATCTGAGATGG 885
Db 781 GTGCAGCAGAGGGGCTGCCCGAGCCCTCATCTGAGATGG 822

RESULT 15
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LOCUS 822 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 2 from Patent EP1245675.
ACCESSION AX552556
VERSION AX552556.1 GI:25896576
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Egawa,K.
TITLE Cancer cell-specific hla-f antigen and a diagnostic method of
cancer by using thereof
JOURNAL Patent: EP 1245675-A 2 02-OCT-2002;
Egawa, Kohji (JP) ; Medinet Co., Ltd. (JP) ; Kimura, Yoshiji (JP)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 124 CGGTACATCGCGTGGAGTACGTAGACGACGCAATTCCTCGCGTTCGACAGGAGCC 183
Db 61 CGGTACATCGCGTGGAGTACGTAGACGACGCAATTCCTCGCGTTCGACAGGAGCC 120

QY 184 GCGATTCCGAGTGGAGCGCGGAGCGGTGGTGGAGCAAGAGGGCGCGCAGTATTGG 243
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Db	241		CTGCTCCGCCCTACAAACAGAGCGAGGCTGGGTCTCACACCTCCAGGGAATGAATGGC	300
Qy	364		TGCGACATGGGCGCCGAGCGACCGCTCCCTCCGCGGGTATCACACGACGCGTACGACGGC	423
Db	301		TGCGACATGGGCGCCGAGCGACCGCTCCCTCCGCGGGTATCACACGACGCGTACGACGGC	360
Qy	424		AAGGATTACATCTCCCTGAACAGAGGACCTGCGGTCTTGACCCGCGCGGACACCGTGGCT	483
Db	361		AAGGATTACATCTCCCTGAACAGAGGACCTGCGGTCTTGACCCGCGCGGACACCGTGGCT	420
Qy	484		CAGATCACCGACGCTTCTATGAGGACAGAGGATATGCAGAGGAGTTTCAGGACCTACCTG	543
Db	421		CAGATCACCGACGCTTCTATGAGGACAGAGGATATGCAGAGGAGTTTCAGGACCTACCTG	480
Qy	544		GAGGCGAGTGCTTGGAGTTGCTCCGACAGATCTTCGAGAAATGGGAAAGAGACGCTACAG	603
Db	481		GAGGCGAGTGCTTGGAGTTGCTCCGACAGATCTTCGAGAAATGGGAAAGAGACGCTACAG	540
Qy	604		CGGCGAGATCTCCAAAGGACACAGCTTGCCACCCACCCCATCTCTGACCATGAGGCCACC	663
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Qy	664		CTGAGGTGCTGGGCCCTTCTACCTTGCGGAGATCACGCTGACCTGGGAGCGGGAT	723
Db	601		CTGAGGTGCTGGGCCCTTCTACCTTGCGGAGATCACGCTGACCTGGGAGCGGGAT	660
Qy	724		GSGGAGGAACAGACCCAGAGACACAGAGCTTGTGGAGACAGGCTGCGAGGGATGGAACC	783
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Qy	784		TTCAGAAATGGGCGGCTGTGGTGGTCCCTTCTGGAGAGGAACAGAGATACACATGCCAT	843
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Qy	844		GTGAGCAGCAGGGGCTGCCCGCCCTCATCTCAGATGG	885
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Job time : 5024 secs

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OM nucleic - nucleic search, using sw model

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12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1089	100.0	1089	10	ADP55584	ADP55584 DNA encod
3	1089	100.0	1188	12	ADJ74945	ADJ74945 Marker ge
4	1089	100.0	1188	12	ADJ74851	ADJ74851 Marker ge
5	1089	100.0	1188	12	ADP10447	ADP10447 Reference
6	952	87.4	2034	5	AAS90913	AAS90913 DNA encod
7	952	87.4	2037	5	AAS90740	AAS90740 DNA encod
8	952	87.4	2037	5	ADI21449	ADI21449 Novel hum
9	822	75.5	822	4	AH45556	AH45556 Human can
10	822	75.5	822	10	ADP55585	ADP55585 DNA encod
11	785	72.2	816	3	AACT78195	AACT78195 Human can
12	645	59.2	645	4	AH45557	AH45557 Human can
13	645	59.2	645	10	ADP55586	ADP55586 DNA encod
14	361	33.1	424	3	AAC00215	AAC00215 Human sec
15	355	32.6	487	9	ACH50642	ACH50642 Human mam
16	339	31.1	459	10	ABX74535	ABX74535 Human cDN
17	289	26.5	1096	10	ADI21922	ADI21922 Novel hum
18	279	25.6	4316	5	ABA83122	ABA83122 HLA-Cw ov
19	279	25.6	4316	6	ABN97218	ABN97218 Gene #371
20	279	25.6	4316	10	ADB33954	ADB33954 HLA-F gen
21	277	25.4	3098	4	AAR86871	AAR86871 Human imm

22	277	25.4	3098	4	AAL04024	AAL04024 Human rep
23	277	25.4	3098	5	ABA18125	ABA18125 Human ner
24	277	25.4	3098	5	AAS40421	AAS40421 DNA encod
25	277	25.4	148934	6	ABR83570	ABR83570 Human cDN
26	276	25.3	546	12	ADQ21922	ADQ21922 Human sof
27	272	25.0	907	2	AAZ53005	AAZ53005 Human pro
28	228	20.9	289	12	ACH84959	ACH84959 Human gen
29	228	20.9	552	12	ACH71259	ACH71259 Human gen
30	212	19.5	1414	5	AAS93415	AAS93415 DNA encod
31	104	9.6	240	2	AAT23311	AAT23311 Human gen
32	89	8.2	379	4	AAI90453	AAI90453 Human pol
33	85	7.8	561	6	ABP56008	ABP56008 Human ova
34	73	6.7	274	3	AAZ94614	AAZ94614 HLA-B gen
35	73	6.7	301	4	AAI21448	AAI21448 Probe #11
36	73	6.7	301	4	ABA66506	ABA66506 Human toe
37	73	6.7	301	4	AAI46715	AAI46715 Probe #15
38	73	6.7	301	4	ABA48596	ABA48596 Human bre
39	73	6.7	301	4	ABA33570	ABA33570 Probe #12
40	73	6.7	301	4	AAK40662	AAK40662 Human bon
41	73	6.7	301	4	AAK14929	AAK14929 Human bra
42	73	6.7	301	4	ABS40231	ABS40231 Human liv
43	73	6.7	301	5	AAI07121	AAI07121 Probe #71
44	73	6.7	301	6	ABS14623	ABS14623 Human gen
45	73	6.7	332	4	AAK54319	AAK54319 Human hae

ALIGNMENTS

RESULT 1
AAH45555
ID AAH45555 standard; DNA; 1089 BP.
XX AC AAH45555;
XX DT 12-SEP-2001 (first entry)
XX DE Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 1.
XX KW HLA-F antigen; cancer cell specific; human; ds.
XX OS Homo sapiens.
XX PH Key
XX CDS Location/Qualifiers
FT 1..1089
FT /*tag= a
FT /product= "Cancer cell specific HLA-F antigen"
XX PN JP2001095584-A.
XX PD 10-APR-2001.
XX PF 30-SEP-1999; 99JP-00279566.
XX PR 30-SEP-1999; 99JP-00279566.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA K.
XX DR WPI; 2001-360493/38.
XX DR P-PSDB; AAG64617.
XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX PS Claim 3; Page 8-9; 12pp; Japanese.
XX CC This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents DNA encoding the cancer cell-specific HLA-F antigen

Db 721 TTCAGAGTGGCGCTGTGGTGGCTTCTGGAGAGAACAGAGATACATGCCAT 780

Qy 844 GTGCAGACGAGGGGCTGCCCCAGCCCTCATCTGAGATGG 885

Db 781 GTGCAGACGAGGGGCTGCCCCAGCCCTCATCTGAGATGG 822

RESULT 10

ADP55585

ID ADP55585 standard; DNA; 822 BP.

AC

ADP55585;

DT 12-FEB-2004 (first entry)

DE DNA encoding fragment #1 of human cancer-cell specific HLA-F antigen.

XX Cancer; human leukocyte antigen-F; HLA-F;

KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;

KW major histocompatibility complex; MHC; cancer cell; human; gene; ds.

XX Homo sapiens.

OS

PH Key Location/Qualifiers

FT 1..822

FT /tag=a

FT /partial

FT /note="This sequence lacks both start and stop codons"

XX JP2003012544-A.

PN

PD 15-JAN-2003.

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PF 27-MAR-2002; 2002JP-00089991.

XX

PR 27-MAR-2001; 2001JP-00090121.

XX

PA (EGAW/) EGAWA K.

PA (MEDI-) MEDINET KK.

PA (KIMU/) KIMURA Y.

XX

DR WPI: 2003-486263/46.

DR P-PSDB; ADP55588.

XX

PT Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.

XX

PS Disclosure; SEQ ID NO 2; 19pp; Japanese.

XX

CC The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence encodes part of the human cancer-cell specific HLA-F antigen.

XX

SQ Sequence 822 BP; 174 A; 250 C; 273 G; 125 T; 0 U; 0 Other;

Query Match 75.5%; Score 822; DB 10; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 GCCTCCCACTCTTGGAGTATTTCAGACCGCTGTGTCCGCGCCCGCGCGGAGGCC 123

Db 1 GCCTCCCACTCTTGGAGTATTTCAGACCGCTGTGTCCGCGCCCGCGCGGAGGCC 60

Qy 124 GCCTACATCGCGGTGGAGTACGTAGACGACACGCAATTCCTGGGGTTCCGACGACGCC 183

Db 61 CGCTACATCGCGTGGAGTACGTAGACGACACGCAATTCCTGCGTTCGACAGCGGCC 120

Qy 184 GCGATTCGAGATGAGACCGCGGAGCCGTGGTGGAGCAGAGGCGCGCGATTTGG 243

Db 121 GCGATTCGAGATGAGACCGCGGAGCCGTGGTGGAGCAGAGGCGCGCGATTTGG 180

Qy 244 GAGTGACACACAGGGGTACGCCAAGGCCAAACGACAGAGTACCGAGTGGCCCTCAGGAAC 303

Db 181 GAGTGACACACAGGGGTACGCCAAGGCCAAACGACAGAGTACCGAGTGGCCCTCAGGAAC 240

Qy 304 CTGCTCCGCGCTCAACACAGAGAGAGCTGGGTCTCACACCTCCAGGGAATGATGGC 363

Db 241 CTGCTCCGCGCTCAACACAGAGAGAGCTGGGTCTCACACCTCCAGGGAATGATGGC 300

Qy 364 TCGACATCGGCGCCGCGACGCGCTCTCCGCGGGTATCACACGACGCGCTACGCGCC 423

Db 301 TCGACATCGGCGCCGCGACGCGCTCTCCGCGGGTATCACACGACGCGCTACGCGCC 360

Qy 424 AAGGATTACATCTCCCTGAAACGAGACCTGCGCTCTGGACCGCGCGGACACCGTGGCT 483

Db 361 AAGGATTACATCTCCCTGAAACGAGACCTGCGCTCTGGACCGCGCGGACACCGTGGCT 420

Qy 484 CAGATCACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGAGTTTCAGGACCTACCTG 543

Db 421 CAGATCACCCAGCGCTTCTATGAGCAGAGGAATATGACAGAGGAGTTTCAGGACCTACCTG 480

Qy 544 GAGGCGAGTGGCTGAGTTCCTCGAGATACCTTGGAGATGGAGAGAGAGCGCTACAG 603

Db 481 GAGGCGAGTGGCTGAGTTCCTCGAGATACCTTGGAGATGGAGAGAGAGCGCTACAG 540

Qy 604 CGCGCAGATCTCCAAAGGACACAGTTCGCCACACACCCCATCTCTGACCATGAGGCCACC 663

Db 541 CGCGCAGATCTCCAAAGGACACAGTTCGCCACACACCCCATCTCTGACCATGAGGCCACC 600

Qy 664 CTGAGTGTGCTGGCGCTTCTACCTCGGAGATCAGCTGACCTGGCGAGCGGAT 723

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Qy 724 GGGGAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACACCGCTCGAGGGGATGGAACC 783

Db 661 GGGGAGGAAACAGACCCAGGACACAGAGCTTGTGGAGACACCGCTCGAGGGGATGGAACC 720

Qy 784 TTCCAGAGTGGCGCTGTGTGTGCTGCTTCTGGAGAGGACAGAGATACATGCCAT 843

Db 721 TTCCAGAGTGGCGCTGTGTGTGCTGCTTCTGGAGAGGAAACAGATACATGCCAT 780

Qy 844 GTGCAGACGAGGGGCTGCCCGCCCTCATCTCTGAGATGG 885

Db 781 GTGCAGACGAGGGGCTGCCCGCCCTCATCTCTGAGATGG 822

RESULT 11

AAC78195

ID AAC78195 standard; cDNA; 816 BP.

XX

AC AAC78195;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human cancer associated gene sequence SEQ ID NO:589.

XX

KW Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnary; immunomodulator; antiinfective; antitumor; antirheumatic; antidiabetic; antitumor; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nontoxic; vasorelaxant; antiproliferative; angiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.

XX

CC This invention relates to a cancer cell specific HLA-F antigen. The
 CC invention includes DNA encoding the antigen, and a method for the
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
 CC used in a method to diagnose cancer, in which the protein is used to
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
 CC sequence represents DNA encoding the cancer cell-specific HLA-F antigen
 CC of the invention
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 SQ Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;

Query Match 59.2%; Score 645; DB 4; Length 645;
 Best Local Similarity 100.0%; Pred. No. 9e-296;
 Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 189
 DB 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 60

QY 190 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGACAAAGAGGCGCCGAGTATGGAGTGG 249
 DB 61 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGACAAAGAGGCGCCGAGTATGGAGTGG 120

QY 250 ACCCAGGCTACGCCAAGGCCCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 309
 DB 121 ACCCAGGCTACGCCAAGGCCCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 180

QY 310 CGCGCTACAAACGAGCGAGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGAC 369
 DB 181 CGCGCTACAAACGAGCGAGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGAC 240

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 DB 241 ATGGGGCCCGAGCGAGCTCTCCGCGGTATCCACGACGCGCTACGACGCGCAAGGAT 300

QY 430 TACATCTCCCTGAACGAGGACCTGGCTCCGCGGCGGACACCTGCTCAGATC 489
 DB 301 TACATCTCCCTGAACGAGGACCTGGCTCCGCGGCGGACACCTGCTCAGATC 360

QY 490 ACCCAGGCTCTTATGAGGACGAGGAATATGACGAGGAGTTCAGGACCTACCTGGAGGC 549
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QY 550 GAGTCCCTGGAGTGTCTCCGAGATATCTGGAGAAATGGAGAGACGCTACAGCGGCA 609
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QY 610 GATCCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 669
 DB 481 GATCCTCCAAAGGCACACGTTGCCACACCCCATCTCTGACCATGAGGCCACCTGAGG 540

QY 670 TGTGGGCGCTGGGTTTACCTCTGGGAGATACGCTGACCTGGAGCGGATGGGAG 729
 DB 541 TGTGGGCGCTGGGTTTACCTCTGGGAGATACGCTGACCTGGAGCGGATGGGAG 600

QY 730 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGACGG 774
 DB 601 GAACAGACCCAGGACACAGAGCTTGTGGAGACAGGCGCTGACGG 645

RESULT 13
 ADF5586
 ID ADF5586 standard; DNA; 645 BP.
 XX
 AC ADF5586;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE DNA encoding fragment #2 of human cancer-cell specific HLA-F antigen.
 XX
 KW Cancer; human leukocyte antigen-F; HLA-F;
 KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 KW major histocompatibility complex; MHC; cancer cell; human; gene; ds.
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OS Homo sapiens.
 XX Key Location/Qualifiers
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 FT /note="This sequence lacks both start and stop codons"
 XX
 PN JP2003012544-A.
 XX
 XX 15-JAN-2003.
 XX
 XX 27-MAR-2002; 2002JP-00088991.
 XX
 XX 27-MAR-2001; 2001JP-00090121.
 PR (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (XIMU/) KIMURA Y.
 XX
 DR WPI; 2003-486263/46.
 DR P-PSDB; ADF5586.
 XX
 XX Agent for preventing and treating cancer, comprising human leukocyte
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 XX
 XX Disclosure; SEQ ID NO 3; 19pp; Japanese.
 XX
 XX The present invention relates to an agent for preventing or treating
 CC cancer. The agent comprises a portion or a complete sequence of a human
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is
 CC unrestricted to the major histocompatibility complex (MHC) and specific
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
 CC is useful for treating or preventing cancer. A cell capable of presenting
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
 CC for diagnosing cancer. The present sequence encodes part of the human
 CC cancer-cell specific HLA-F antigen.
 XX
 SQ Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;

Query Match 59.2%; Score 645; DB 10; Length 645;
 Best Local Similarity 100.0%; Pred. No. 9e-296;
 Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 189
 DB 1 ATCCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCGACGCGACCGCGGATT 60

QY 190 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGACAAAGAGGCGCCGAGTATGGAGTGG 249
 DB 61 CCGAGGATGGAGCCCGCGGAGCCGCTGGTGGACAAAGAGGCGCCGAGTATGGAGTGG 120

QY 250 ACCCAGGCTACGCCAAGGCCCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 309
 DB 121 ACCCAGGCTACGCCAAGGCCCAACGACACACTGACGAGTGGCCCTGAGGAACCTGCTC 180

QY 310 CGCGCTACAAACGAGCGAGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGAC 369
 DB 181 CGCGCTACAAACGAGCGAGCTGGGTCTCACACCTCCAGGGAATGAATGGCTGGAC 240

QY 370 ATGGGGCCCGAGCGAGCTCTCCGCGGCGGACACCTGCTCAGATC 429
 DB 241 ATGGGGCCCGAGCGAGCTCTCCGCGGCGGACACCTGCTCAGATC 300

QY 430 TACATCTCCCTGAACGAGGACCTGGCTCCGCGGCGGACACCTGCTCAGATC 489
 DB 301 TACATCTCCCTGAACGAGGACCTGGCTCCGCGGCGGACACCTGCTCAGATC 360

QY 490 ACCCAGGCTCTTATGAGGACGAGGAATATGACGAGGAGTTCAGGACCTACCTGGAGGC 549
 DB 361 ACCCAGGCTCTTATGAGGACGAGGAATATGACGAGGAGTTCAGGACCTACCTGGAGGC 420

CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX
 SQ Sequence 487 BP; 97 A; 154 C; 159 G; 73 T; 0 U; 4 Other;

Query Match 32.6%; Score 355; DB 9; Length 487;
 Best Local Similarity 100.0%; Pred. No. 4.4e-158;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	144	CGTAGACACACGCAATTCCTGGGTTCCGAGCAGCGCGGATTCGAGGATGGAGCC	203
DB	132	CGTAGACACACGCAATTCCTGGGTTCCGAGCAGCGCGGATTCGAGGATGGAGCC	191
QY	204	CGGGAGCCGTGGGTGGAGCAAGAGGGCCGCGAGTATGGGAGTGGACACAGGGTACGC	263
DB	192	CGGGAGCCGTGGGTGGAGCAAGAGGGCCGCGAGTATGGGAGTGGACACAGGGTACGC	251
QY	264	CAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTCCGCCGCTACAAACA	323
DB	252	CAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGGAACCTGCTCCGCCGCTACAAACA	311
QY	324	GAGCGAGCCTGGGTCTCACACCTCCAGGGAATGATGGCTCGGACATGGGCCCGAGCG	383
DB	312	GAGCGAGCCTGGGTCTCACACCTCCAGGGAATGATGGCTCGGACATGGGCCCGAGCG	371
QY	384	ACGCCTCCTCCGCGGGTATCACCAGCACGCGGTACGACGCGCAAGGATTACATCTCCCTGAA	443
DB	372	ACGCCTCCTCCGCGGGTATCACCAGCACGCGGTACGACGCGCAAGGATTACATCTCCCTGAA	431
QY	444	CGAGGACCTGGCTCTCGACCGCGCGGACACCGTGGCTCAGATCACCACGCG	498
DB	432	CGAGGACCTGGCTCTCGACCGCGCGGACACCGTGGCTCAGATCACCACGCG	486

Search completed: December 16, 2004, 13:07:23
 Job time : 637 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:56:48 ; Search time 120 Seconds
(without alignments)
6450.409 Million cell updates/sec

Title: US-09-819-371-1

Perfect score: 1089

Sequence: 1 atgggccccgaagcctcct.....tcacagtaataaagtgtga 1089

Scoring table: OLIGO_NVC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	33.1	424	US-09-513-999C-213	Sequence 213, App
2	73	6.7	1221	US-09-799-451-322	Sequence 322, App
3	73	6.7	1521	US-09-566-921-130	Sequence 130, App
4	73	6.7	1559	US-09-799-451-317	Sequence 317, App
5	73	6.7	6553	US-08-522-942-1	Sequence 1, Appli
6	65	6.0	152	US-09-513-999C-12022	Sequence 12022, A
7	61	5.6	2225	US-09-799-451-318	Sequence 318, App
8	61	5.6	3520	US-09-220-132-84	Sequence 84, Appl
9	52	4.8	2825	US-09-799-451-318	Sequence 318, App
10	52	4.8	4059	US-08-564-313-2	Sequence 2, Appli
11	52	4.8	4059	PCT-US94-06069-2	Sequence 2, Appli
12	52	4.8	4965	US-08-564-313-1	Sequence 1, Appli
13	52	4.8	4965	PCT-US94-06069-1	Sequence 1, Appli
14	50	4.6	371	US-08-403-853-13	Sequence 13, Appl
15	50	4.6	438	US-09-397-787-329	Sequence 329, App
16	50	4.6	1183	US-09-028-045-11	Sequence 11, Appl
17	50	4.6	1183	US-09-435-321-11	Sequence 11, Appl
18	44	4.0	1491	US-09-799-451-324	Sequence 324, App
19	43	3.9	1100	US-09-799-451-320	Sequence 320, App
20	42	3.9	844	US-09-404-879A-132	Sequence 132, App
21	42	3.9	844	US-09-338-933-132	Sequence 132, App
22	42	3.9	844	US-09-215-681-132	Sequence 132, App
23	42	3.9	844	US-09-215-003A-132	Sequence 132, App
24	42	3.9	844	US-09-667-857-132	Sequence 132, App
25	41	3.8	293	US-08-263-413-3	Sequence 3, Appli
26	41	3.8	297	US-08-263-413-4	Sequence 4, Appli
27	40	3.7	276	US-08-127-954-134	Sequence 134, App

28 40 3.7 276 3 US-08-577-081A-40 Sequence 40, Appl
29 40 3.7 439 4 US-09-513-999C-11566 Sequence 11566, A
30 40 3.7 1086 4 US-08-914-372C-2 Sequence 2, Appli
31 40 3.7 1095 4 US-08-914-372C-4 Sequence 4, Appli
32 40 3.7 1095 4 US-08-914-372C-6 Sequence 6, Appli
33 40 3.7 1095 4 US-08-914-372C-36 Sequence 36, Appl
34 40 3.7 1310 4 US-09-799-451-325 Sequence 325, App
35 40 3.7 1546 4 US-09-443-199C-1114 Sequence 1114, Ap
36 39 3.6 51 4 US-08-914-372C-1 Sequence 1, Appli
37 39 3.6 1086 4 US-08-914-372C-3 Sequence 3, Appli
38 39 3.6 1086 4 US-08-914-372C-35 Sequence 35, Appl
39 39 3.6 1086 4 US-08-914-372C-5 Sequence 5, Appli
40 39 3.6 1095 4 US-09-702-705-1087 Sequence 1087, Ap
41 33 3.0 329 4 US-09-736-457-1087 Sequence 1087, Ap
42 33 3.0 329 4 US-09-614-124B-1087 Sequence 1087, Ap
43 33 3.0 329 4 US-09-671-325-1087 Sequence 1087, Ap
44 33 3.0 329 4 US-09-658-824-1087 Sequence 1087, Ap
45 33 3.0 329 4 US-09-658-824-1087 Sequence 1087, Ap

ALIGNMENTS

RESULT 1

US-09-513-999C-213
; Sequence 213, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 213
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64...423
; NAME/KEY: sig_peptide
; LOCATION: 64...114
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SILLILLSGALALT/DT

US-09-513-999C-213

Query Match 33.1%; Score 361; DB 4; Length 424;

Best Local Similarity 100.0%; Pred. No. 2.1e-161;

Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCCCCGAGCCTCCTCTGCTCTCAGGGGCCCTGCGCCCTGACCGATCTTGG 60

64 ATGGGCCCCGAGCCTCCTCTGCTCTCAGGGGCCCTGCGCCCTGACCGATCTTGG 123

QY 61 CGGGCTCCCACTCCTTTAGGTATTTTCAGCACCGCTGTGTGCGGCCCGCGCGGGAG 120

124 CGGGCTCCCACTCCTTTAGGTATTTTCAGCACCGCTGTGTGCGGCCCGCGCGGGAG 183

QY 121 CCCCGCTACATCGCGGTGGAGTAGTAGACACCGCATTCCTGGTTCGACCGAC 180

184 CCCCGCTACATCGCGGTGGAGTAGTAGACACCGCATTCCTGGTTCGACCGAC 243

QY 181 CCGCGATTCCGAGATGAGCGCGGAGCCCGTGGTGGAGCAAGAGGGCGCGCAGTAT 240

244 CCGCGATTCCGAGATGAGCGCGGAGCCCGTGGTGGAGCAAGAGGGCGCGCAGTAT 303

QY 241 TGGAGTGGACACAGGTACGCCAAGCCACAGACCTACCGAGTGGCCCTGAGG 300
Db 304 TGGAGTGGACACAGGTACGCCAAGCCACAGACCTACCGAGTGGCCCTGAGG 363
QY 301 AACCTGCTCCGCGCTCAACACAGAGCGAGGCTGGGTCTCACACCCCTCCAGGGAATGAAT 360
Db 364 AACCTGCTCCGCGCTCAACACAGAGCGAGGCTGGGTCTCACACCCCTCCAGGGAATGAAT 423
QY 361 G 361
Db 424 G 424

RESULT 2

US-09-799-451-322
Sequence 322, Application US/09799451

Patent No. 6783969

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Asundi, Vinod

APPLICANT: Ren, Feiyan

APPLICANT: Zhang, Jie

APPLICANT: Xue, Aidong J.

APPLICANT: Zhao, Qing A.

APPLICANT: Wang, Jian-Rui

APPLICANT: Ma, Yungqing

APPLICANT: Yamazaki, Victoria

APPLICANT: Chen, Rui-hong

APPLICANT: Wang, Zhiwei

APPLICANT: Wang, Dunrui

APPLICANT: Yang, Yonghong

APPLICANT: Wehrman, Tom

APPLICANT: Ghosh, Reena

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6783969el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 803

CURRENT APPLICATION NUMBER: US/09/799,451

CURRENT FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 948

SOFTWARE: pt_FL_Genes Version 2.0

SEQ ID NO 322

LENGTH: 1221

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(213)

US-09-799-451-322

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691

Db 769 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 828

QY 692 CTGCGGAGATCAC 704

Db 829 CTGCGGAGATCAC 841

RESULT 3

US-09-566-921-130

Sequence 130, Application US/09566921

Patent No. 6682888

GENERAL INFORMATION:

APPLICANT: Loring, Jeanne F.

APPLICANT: Tingley, Debora W.

APPLICANT: Edwards, Carla M.

TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

FILE REFERENCE: PA-0024 US

CURRENT APPLICATION NUMBER: US/09/566,921

CURRENT FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL Program

SEQ ID NO 130

LENGTH: 1521

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6682888 1040429.6

US-09-566-921-130

Query Match

Best Local Similarity 100.0%; Pred. No. 5.3e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691

Db 645 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 704

QY 692 CTGCGGAGATCAC 704

Db 705 CTGCGGAGATCAC 717

RESULT 4

US-09-799-451-317

Sequence 317, Application US/09799451

Patent No. 6783969

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Asundi, Vinod

APPLICANT: Ren, Feiyan

APPLICANT: Zhang, Jie

APPLICANT: Xue, Aidong J.

APPLICANT: Zhao, Qing A.

APPLICANT: Wang, Jian-Rui

APPLICANT: Ma, Yungqing

APPLICANT: Yamazaki, Victoria

APPLICANT: Chen, Rui-hong

APPLICANT: Wang, Zhiwei

APPLICANT: Wang, Dunrui

APPLICANT: Yang, Yonghong

APPLICANT: Wehrman, Tom

APPLICANT: Ghosh, Reena

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6783969el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 803

CURRENT APPLICATION NUMBER: US/09/799,451

CURRENT FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 948

SOFTWARE: pt_FL_Genes Version 2.0

SEQ ID NO 317

LENGTH: 1559

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (43)..(681)

US-09-799-451-317

Query Match

Best Local Similarity 100.0%; Pred. No. 5.3e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691

Db 685 CCACACCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTTACC 744
QY 692 CTGCGGAGATCAC 704
Db 745 CTGCGGAGATCAC 757

RESULT 5
US-08-522-942-1
; Sequence 1, Application US/08522942
; Patent No. 5753442
; GENERAL INFORMATION:
; APPLICANT: Tyan, Dolly B.
; TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC
; TITLE OF INVENTION: PREPOSITION FOR SERONEGATIVE SPONDYLOARTHRITIS AND
; TITLE OF INVENTION: PRODUCTS THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4365 Executive Drive, Suite 1500
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P07 33624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-1995
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-522-942-1

Query Match 6.7%; Score 73; DB 1; Length 653;
Best Local Similarity 100.0%; Pred. No. 5e-25;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACACCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTTACC 691
Db 2269 CCACACCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTTACC 2328

QY 692 CTGCGGAGATCAC 704
Db 2329 CTGCGGAGATCAC 2341

RESULT 6
US-09-513-999C-12022
; Sequence 12022, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12022
; LENGTH: 152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-12022

Query Match 6.0%; Score 65; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCCCCGAGCCCTCTCTGCTCTCTGAGGGCCCTGCGCCCTGACCGATCTTGG 60
Db 64 ATGGGCCCCGAGCCCTCTCTGCTCTCTGAGGGCCCTGCGCCCTGACCGATCTTGG 123
QY 61 GCGGG 65
Db 124 GCGGG 128

RESULT 7
US-09-799-451-318/c
; Sequence 318, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Resna
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 318
; LENGTH: 2225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)..(1769)
US-09-799-451-318

Query Match 5.6%; Score 61; DB 4; Length 2225;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 TCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTTGTACCTTGGGAGATCA 703
Db 449 TCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTTGTACCTTGGGAGATCA 390

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QY 704 C 704
Db 389 C 389

RESULT 8
US-09-220-132-84
; Sequence 84, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 3520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-84

Query Match 5.6%; Score 61; DB 4; Length 3520;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 TCTCTGACCATGAGGCCACCCCTGAGTGTCTGGGCCCTTCTACCTCGCGAGATCA 703
Db 1690 TCTCTGACCATGAGGCCACCCCTGAGTGTCTGGGCCCTTCTACCTCGCGAGATCA 1749

QY 704 C 704
Db 1750 C 1750

RESULT 9
US-09-799-451-318
; Sequence 318, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 318
; LENGTH: 2225
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)..(1769)
US-09-799-451-318

Query Match 4.8%; Score 52; DB 4; Length 2225;
Best Local Similarity 100.0%; Pred. No. 4.6e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGTGTCTGGCCCTGGG 683
Db 1773 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGTGTCTGGCCCTGGG 1824

RESULT 10
US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92860
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7
US-08-564-313-2

Query Match 4.8%; Score 52; DB 2; Length 4059;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCCCTGAGTGTCTGGCCCTGGG 683
```

Db 2243 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 2192

RESULT 11

PCT-US94-06069-2/c
; Sequence 2, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7
; PCT-US94-06069-2

Query Match 4.8%; Score 52; DB 5; Length 4059;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 683
Db 2243 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 2192

RESULT 12

US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary

; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7 and Beta-2
; US-08-564-313-1

Query Match 4.8%; Score 52; DB 2; Length 4965;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 683
Db 1175 CCCACACCCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGG 1226

RESULT 13

PCT-US94-06069-1
; Sequence 1, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033VPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1

Query Match 4.8%; Score 52; DB 5; Length 4965;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 CCCACCCCATCTTGACCATGAGCCACCTCGAGGTCTGGCCCTGGG 683
Db 1175 CCCACCCCATCTTGACCATGAGCCACCTCGAGGTCTGGCCCTGGG 1226

RESULT 14
US-08-403-853-13
Sequence 13, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
APPLICANT: LAH, Maria
APPLICANT: KORRT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: KIWELL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..363
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
US-08-403-853-13

Query Match 4.6%; Score 50; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 748 GAGCTTGTGGAGACCCAGGCGCTGCAGGGGATGGAACCTTCCAGAGTGGGC 797
Db 196 GAGCTTGTGGAGACCCAGGCGCTGCAGGGGATGGAACCTTCCAGAGTGGGC 245

RESULT 15
US-09-397-787-329
Sequence 329, Application US/09397787
Patent No. 6468758
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 329
LENGTH: 438
TYPE: DNA
ORGANISM: Homo sapien
US-09-397-787-329

Query Match 4.6%; Score 50; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 748 GAGCTTGTGGAGACCCAGGCGCTGCAGGGGATGGAACCTTCCAGAGTGGGC 797
Db 158 GAGCTTGTGGAGACCCAGGCGCTGCAGGGGATGGAACCTTCCAGAGTGGGC 207

Search completed: December 16, 2004, 17:03:52
Job time: 122 secs

181 GCGCGATTCGAGATGAGCCGCGGAGCCGCTGGTGGAGCAAGAGGGGCGCAGTAT 240
 181 GCGCGATTCGAGATGAGCCGCGGAGCCGCTGGTGGAGCAAGAGGGGCGCAGTAT 240
 241 TGGGAGTGAGCACACAGGAGTACGCAAGGCAAGCAGACAGACTACCGAGTGGCCCTGAGG 300
 241 TGGGAGTGAGCACACAGGAGTACGCAAGGCAAGCAGACAGACTACCGAGTGGCCCTGAGG 300
 301 AACCTGCTCCGCGCTACCAACAGAGAGGCTGGGTCTCACACCTTCCAGGGAATGAAT 360
 301 AACCTGCTCCGCGCTACCAACAGAGAGGCTGGGTCTCACACCTTCCAGGGAATGAAT 360
 361 GGTCTCGACATGCGGCGCCGCGGAGCGCTCTCCGCGGTATCACACGACGCGTACGAC 420
 361 GGTCTCGACATGCGGCGCCGCGGAGCGCTCTCCGCGGTATCACACGACGCGTACGAC 420
 421 GCGAGGATTAATCTCCCTGAAAGAGAGCTCGCTCTGGACCGCGGCGGACACCGTG 480
 421 GCGAGGATTAATCTCCCTGAAAGAGAGCTCGCTCTGGACCGCGGCGGACACCGTG 480
 481 GGTCTCGACATGCGGCGCCGCGGAGCGCTCTCCGCGGTATCACACGACGCGTACGAC 540
 481 GGTCTCGACATGCGGCGCCGCGGAGCGCTCTCCGCGGTATCACACGACGCGTACGAC 540
 541 CTGAGGCGAGTGCCTGGAGTCTCCGAGAGTCTGGAGATTTGGAGATGGAGAGAGCGTA 600
 541 CTGAGGCGAGTGCCTGGAGTCTCCGAGAGTCTGGAGATTTGGAGATGGAGAGAGCGTA 600
 601 CAGCGCGAGATCTCCAAAGGCAACGTTGCGGAGTCTGGAGATTTGGAGATGGAGAGAGCGTA 660
 601 CAGCGCGAGATCTCCAAAGGCAACGTTGCGGAGTCTGGAGATTTGGAGATGGAGAGAGCGTA 660
 661 ACCCTGAGTGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGACGCGG 720
 661 ACCCTGAGTGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGACGCGG 720
 721 GATGGGAGGAAACAGACCCAGACAGAGTGTGGAGACCGAGCTGCGAGGAGATGA 780
 721 GATGGGAGGAAACAGACCCAGACAGAGTGTGGAGACCGAGCTGCGAGGAGATGA 780
 781 ACCTTCCAGAGTGGGCGCTGGTGTGCTTCTGGAGAGGAAACAGAGATACATGC 840
 781 ACCTTCCAGAGTGGGCGCTGGTGTGCTTCTGGAGAGGAAACAGAGATACATGC 840
 841 CATGTGACAGCAGAGGCTGCCCGCCCTCATCTCGAGTGGAGAGTCTCCCGAG 900
 841 CATGTGACAGCAGAGGCTGCCCGCCCTCATCTCGAGTGGAGAGTCTCCCGAG 900
 901 CCCACATCCCATCTGGGCTATGTTGCTGGGCTTGTCTTGGAGCTGGTCACT 960
 901 CCCACATCCCATCTGGGCTATGTTGCTGGGCTTGTCTTGGAGCTGGTCACT 960
 961 GGAGCTGTGGTCTGCTGTGATGTGAGAGAGAGCTCAGATGAACAGAGAGGAGC 1020
 961 GGAGCTGTGGTCTGCTGTGATGTGAGAGAGAGCTCAGATGAACAGAGAGGAGC 1020
 1021 TACTCTCAGGCTGAGTCACTGACAGTGGCGGCTCTGGGCTGTCTCTCAGAGTAAT 1080
 1021 TACTCTCAGGCTGAGTCACTGACAGTGGCGGCTCTGGGCTGTCTCTCAGAGTAAT 1080
 1081 AAAGTGTA 1089
 1081 AAAGTGTA 1089

RESULT 2

US-10-172-118-1806
 ; Sequence 1806, Application US/10172118
 ; Publication No. US20030224374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter

APPLICANT: Mao, Mao
 APPLICANT: Roberts, Chris
 APPLICANT: Van't Veer, Laura
 APPLICANT: Van de Vijver, Marc
 APPLICANT: Bernards, Rene
 TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 FILE REFERENCE: 9301-175-999
 CURRENT APPLICATION NUMBER: US/10/172,118
 CURRENT FILING DATE: 2002-06-14
 PRIOR APPLICATION NUMBER: 60/380,770
 PRIOR FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 2699
 SEQ ID NO 1806
 LENGTH: 1188
 TYPE: DNA
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: NM 018950
 DATABASE ENTRY DATE: 2001-06-18
 US-10-172-118-1806

Query Match 100.0%; Score 1089; DB 15; Length 1188;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGCCCGGAGCCTCTCTGCTCTCAGGGGCGCTGGCCCTGACCGGATCTTGG 60
 Db 1 ATGCGCCCGGAGCCTCTCTGCTCTCAGGGGCGCTGGCCCTGACCGGATCTTGG 60
 Qy 61 GCGGGTCCCACTCTCTGAGTATTTAGCAACCGCTGTCTCGCGCCCGCGGGGAG 120
 Db 61 GCGGGTCCCACTCTCTGAGTATTTAGCAACCGCTGTCTCGCGCCCGCGGGGAG 120
 Qy 121 CCCCGTACATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCAGACGAC 180
 Db 121 CCCCGTACATCGCGTGGAGTACGTAGACGACGCAATTCCTCGGTTCCAGACGAC 180
 Qy 181 GCGCGCATCCGAGGATGGAGCCGCGGAGCGCTGGTGGAGCAAGAGGGCGCAGTAT 240
 Db 181 GCGCGCATCCGAGGATGGAGCCGCGGAGCGCTGGTGGAGCAAGAGGGCGCAGTAT 240
 Qy 241 TGGGAGTGACACACAGGCTACGCCAAGGCAAGCAGACAGCTACCGAGTGGCCCTGAGG 300
 Db 241 TGGGAGTGACACACAGGCTACGCCAAGGCAAGCAGACAGCTACCGAGTGGCCCTGAGG 300
 Qy 301 AACCTGCTCCGCGCTTACAAACAGAGAGGCTGGGTCTCACACCTTCCAGGGAATGAAT 360
 Db 301 AACCTGCTCCGCGCTTACAAACAGAGAGGCTGGGTCTCACACCTTCCAGGGAATGAAT 360
 Qy 361 GGTCTGACATGCGGCGCCGAGCGCTCTCTCGCGGTATCACACGACGCGTACGAC 420
 Db 361 GGTCTGACATGCGGCGCCGAGCGCTCTCTCGCGGTATCACACGACGCGTACGAC 420
 Qy 421 GGCAAGATTAATCTCTCTGAAAGAGAGCTGGCTCTCTGGAACCGCGGAGACCGCTG 480
 Db 421 GGCAAGATTAATCTCTCTGAAAGAGAGCTGGCTCTCTGGAACCGCGGAGACCGCTG 480
 Qy 481 GCTCAGATCAACCGAGCGCTTCTATGAGGCAAGAGATATGAGAGGAGTTCAGGACCTAC 540
 Db 481 GCTCAGATCAACCGAGCGCTTCTATGAGGCAAGAGATATGAGAGGAGTTCAGGACCTAC 540
 Qy 541 CTGAGGGGAGTGCCTGGAGTGTCTCGCAGATACCTTGGAGATGGAGAGAGCGCTA 600
 Db 541 CTGAGGGGAGTGCCTGGAGTGTCTCGCAGATACCTTGGAGATGGAGAGAGCGCTA 600
 Qy 601 CAGCGCGAGATCTCCAAAGGCAACGTTGCGGAGTCTGGAGATTTGGAGAGAGCGG 660
 Db 601 CAGCGCGAGATCTCCAAAGGCAACGTTGCGGAGTCTGGAGATTTGGAGAGAGCGG 660
 Qy 661 ACCCTGAGTGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGACGCGG 720
 Db 661 ACCCTGAGTGTGGGCGCTGGGCTTCTACCTGCGGAGATCACGCTGACCTGACGCGG 720

[REDACTED]

Db 754 GGAGAGGAACAGAGATACATGCCATGTGACGACGAGGGGCTGCCCCAGCCCTCATC 813

Qy 877 CTGAGATGG 885
 |||||
 Db 814 CTGAGATGG 822

RESULT 6

US-09-819-371-3
 ; Sequence 3, Application US/09819371
 ; Publication No. US20040053344A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 645
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-819-371-3

Query Match 45.3%; Score 493; DB 11; Length 645;

Best Local Similarity 99.7%; Pred. No. 3.3e-246;
 Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	180	CGCGCGGATTCGAGGATGAGCGCGGAGCGCGGTGGAGCAAGAGGGCGCGAGTA	239
Db	51	CGCGCGGATTCGAGGATGAGCGCGGAGCGCGGTGGAGCAAGAGGGCGCGAGTA	110
Qy	240	TTGGAGTGGACACAGGCTAGCCAGGCGGAGCGCGGTGGAGCAAGAGGGCGCGAGTA	299
Db	111	TTGGAGTGGACACAGGCTAGCCAGGCGGAGCGCGGTGGAGCAAGAGGGCGCGAGTA	170
Qy	300	GAACCTGCTCCGCGGTACAAACAGAGGAGGCTGGGTCTCACACCTCTCCAGGGAATGAA	359
Db	171	GAACCTGCTCCGCGGTACAAACAGAGGAGGCTGGGTCTCACACCTCTCCAGGGAATGAA	230
Qy	360	TGGCTGGACATGGGCGCGGAGCGGCTCTCCGCGGTATACAGACGCGTACGA	419
Db	231	TGGCTGGACATGGGCGCGGAGCGGCTCTCCGCGGTATACAGACGCGTACGA	290
Qy	420	CGCAAGGATTAATCTCCCTGAACAGAGACCTGCGCTCTCCGCGGTATACAGACGCGTACGA	479
Db	291	CGCAAGGATTAATCTCCCTGAACAGAGACCTGCGCTCTCCGCGGTATACAGACGCGTACGA	350
Qy	480	GGCTCAGATACCCAGCGCTTCTATGAGCAGAGGAATATGAGAGGATTCAGGACCTA	539
Db	351	GGCTCAGATACCCAGCGCTTCTATGAGCAGAGGAATATGAGAGGATTCAGGACCTA	410
Qy	540	CTTGAGGCGGAGTGGCTGCTCGGAGTGTCTCGGAGATCTTGAGGAATGGAGAGAGCGT	599
Db	411	CTTGAGGCGGAGTGGCTGCTCGGAGTGTCTCGGAGTGTCTTGAGGAATGGAGAGAGCGT	470
Qy	600	ACAGCGCGAGATCTCCAAAGGACACAGTGGCCACACCCATCTGACCATGAGGC	659
Db	471	ACAGCGCGAGATCTCCAAAGGACACAGTGGCCACACCCATCTGACCATGAGGC	530
Qy	660	CACCTGAGTGTGGGCGCTGGGCTTCTACCTCGGAGATACGCTGACCTGGCAGCG	719
Db	531	CACCTGAGTGTGGGCGCTGGGCTTCTACCTCGGAGATACGCTGACCTGGCAGCG	590
Qy	720	GGATGGGAGGACACAGCAGGACACAGAGCTTGTGGAGACCGAGGCTGACGG 774	
Db	591	GGATGGGAGGACACAGCAGGACACAGAGCTTGTGGAGACCGAGGCTGACGG 645	

RESULT 7

US-09-918-995-37854

; Sequence 37854, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 37854
 ; LENGTH: 487
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(487)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-918-995-37854

Query Match 32.6%; Score 355; DB 10; Length 487;

Best Local Similarity 100.0%; Pred. No. 2.7e-174;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	144	CGTAGACACACGCAATCTCGGTTCGACAGCGCGCGGATTCGAGGATGGAGCC	203
Db	132	CGTAGACACACGCAATCTCGGTTCGACAGCGCGCGGATTCGAGGATGGAGCC	191
Qy	204	CGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGACACAGGGTACGC	263
Db	192	CGCGGAGCGGTGGGTGGAGCAAGAGGGCGCGAGTATTGGAGTGACACAGGGTACGC	251
Qy	264	CAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACTGCTCCGCGGTACACCA	323
Db	252	CAAGCCCAACGACAGACTGACCGAGTGGCCCTGAGGAACTGCTCCGCGGTACACCA	311
Qy	324	GAGCGAGGCTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGCACATGGGCGCGGACGG	383
Db	312	GAGCGAGGCTGGGTCTCACACCTCTCCAGGGAATGAATGGCTGCACATGGGCGCGGACGG	371
Qy	384	ACGCTCTCTCGCGGTATACAGACGCGGTACGAGGAGGATATCTCCCTGAA	443
Db	372	ACGCTCTCTCGCGGTATACAGACGCGGTATACAGACGCGGTACGAGGAGGATATCTCCCTGAA	431
Qy	444	CGAGGACCTGGCTCTCTGGACCGCGGACACCGTGGCTCAGATCACCCAGCGC	498
Db	432	CGAGGACCTGGCTCTCTGGACCGCGGACACCGTGGCTCAGATCACCCAGCGC	486

RESULT 8

US-09-880-107-3713
 ; Sequence 3713, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3713
 ; LENGTH: 4316

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X17093
US-09-880-107-3713

Query Match      25.6%; Score 279; DB 9; Length 4316;
Best Local Similarity 100.0%; Pred. No. 7.8e-135;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 CAGATCTCTCCAAAGGACACAGCTTCCGACACACACCCCATCTCTGACCATGAGGCGACCCCTGA 667
DB 2413 CAGATCTCTCCAAAGGACACAGCTTCCGACACACACCCCATCTCTGACCATGAGGCGACCCCTGA 2472
QY 668 GGTGTGGGGCCCTGGGCTTTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGG 727
DB 2473 GGTGTGGGGCCCTGGGCTTTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGG 2532
QY 728 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTCTGAGGGATGGAACCTTCC 787
DB 2533 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTCTGAGGGATGGAACCTTCC 2592
QY 788 AGAAGTGGGGCCCTGGGCTTTGTGTGCTTCTCTGAGAGGAACAGATACATGCCATGTGC 847
DB 2593 AGAAGTGGGGCCCTGGGCTTTGTGTGCTTCTCTGAGAGGAACAGATACATGCCATGTGC 2652
QY 848 AGCAGAGGGGCTGCCCCAGCCCTCATCTGAGATGGG 886
DB 2653 AGCAGAGGGGCTGCCCCAGCCCTCATCTGAGATGGG 2691

RESULT 9
US-10-257-021-81
; Sequence 81, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 4316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-81

Query Match      25.6%; Score 279; DB 15; Length 4316;
Best Local Similarity 100.0%; Pred. No. 7.8e-135;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 CAGATCTCTCCAAAGGACACAGCTTCCGACACACCCCATCTCTGACCATGAGGCGACCCCTGA 667
DB 2413 CAGATCTCTCCAAAGGACACAGCTTCCGACACACCCCATCTCTGACCATGAGGCGACCCCTGA 2472
QY 668 GGTGTGGGGCCCTGGGCTTTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGG 727
DB 2473 GGTGTGGGGCCCTGGGCTTTACCTCGGAGATCAGCTGACCTGGCAGCGGGATGGGG 2532
QY 728 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTCTGAGGGATGGAACCTTCC 787
DB 2533 AGGACACAGCCAGGACACAGAGCTTGTGAGACAGGCTCTGAGGGATGGAACCTTCC 2592
QY 788 AGAAGTGGGGCCCTGGGCTTTGTGTGCTTCTCTGAGAGGAACAGATACATGCCATGTGC 847
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DB 2593 AGAAGTGGGGCCCTGGGCTTTGTGTGCTTCTCTGAGAGGAACAGATACATGCCATGTGC 2652
QY 848 AGCAGAGGGGCTGCCCCAGCCCTCATCTGAGATGGG 886
DB 2653 AGCAGAGGGGCTGCCCCAGCCCTCATCTGAGATGGG 2691

RESULT 10
US-09-764-891-6712
; Sequence 6712, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6712
; LENGTH: 3098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6712

Query Match      25.4%; Score 277; DB 10; Length 3098;
Best Local Similarity 100.0%; Pred. No. 9e-134;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 802 CGGGGTATCACACGAGCAGCGCTAGCGGCAAGATTACATCTCCCTGACGAGGACCTG 861
QY 454 CGCTCTCGACCGCGCGGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGGCGAG 513
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QY 514 GAATATGAGAGGAGCTTCAGACACCTACTGAGGGCGAGTGCTGGAGTTGCTCCGACAG 573
DB 922 GAATATGAGAGGAGTTTCAAGACCTTACTGAGGGCGAGTGCTGGAGTTGCTCCGACAG 981
QY 574 TACTTGGAGATGGGAGGACACGCTTACAGCGGCGAG 610
DB 982 TACTTGGAGATGGGAGGAGGACGCTACAGCGGCGAG 1018

RESULT 11
US-10-091-572-573
; Sequence 573, Application US/10091572
; Publication No. US20030054373A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA118C1
; CURRENT APPLICATION NUMBER: US/10/091,572
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,850
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
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PRIOR FILING DATE: 2000-07-11	PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14	PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07	PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/216,880
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PRIOR FILING DATE: 2000-09-05	

PRIOR APPLICATION NUMBER: 60/236,367	PRIOR FILING DATE: 2000-09-29
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PRIOR APPLICATION NUMBER: 60/240,960	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935	PRIOR FILING DATE: 2000-10-13
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PRIOR APPLICATION NUMBER: 60/241,787	PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474	PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532	PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216	PRIOR FILING DATE: 2000-11-17
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PRIOR APPLICATION NUMBER: 60/226,681	PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182	PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836	PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438	PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135	PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/235,266	PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218	PRIOR FILING DATE: 2000-11-17
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PRIOR APPLICATION NUMBER: 60/249,213	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212	PRIOR FILING DATE: 2000-11-17
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PRIOR APPLICATION NUMBER: 60/249,245	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,244	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,211	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214	PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297	PRIOR FILING DATE: 2000-11-17

Qy	608	CAGATCTCCAAAGGACACACGTTGGCCACACACCCATCTCTGACCAATGAGGCACACCTGA	667
Db	246	CAGATCTCTCCAAAGGACACACGTTGGCCACACACCCATCTCTGACCAATGAGGCACACCTGA	305
Qy	668	GGTGTCTGGGCCCTTGGGCTTCTACCTCTGGGAGATCAACGCTGACCTGGCAGCGGATGGGG	728
Db	306	GGTGTCTGGGCCCTTGGGCTTCTACCTCTGGGAGATCAACGCTGACCTGGCAGCGGATGGGG	365
Qy	728	AGGAACAGACCCAGGACACAGAGCTTTGGAGACCAAGGCTTGAGGGGATGGAACCTTCC	787
Db	366	AGGAACAGACCCAGGACACAGAGCTTTGGAGACCAAGGCTTGAGGGGATGGAACCTTCC	425
Qy	788	AGAACTGGGCCCTGTGTGTGTGTGTCTTGAGAGGAAACAGAGATACATGCCATGTGC	847
Db	426	AGAACTGGGCCCTGTGTGTGTGTGTCTTGAGAGGAAACAGAGATACATGCCATGTGC	485
Qy	848	AGCACGAGGGGTGCCCCAGCCCTTCATCTCTGAGATGGG	886
Db	486	AGCACGAGGGGTGCCCCAGCCCTTCATCTCTGAGATGGG	524

RESULT 14

US-10-264-049-1888
; Sequence 1888, Application US/10264049
; Publication No. US20040005579A1

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APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133PI
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/19569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1888

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7 NAME/KEY: misc_feature
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11 NAME/KEY: misc_feature
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/ US-10-264-049-1888

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Best Local Similarity 99.3%; Pred. No. 1.2e-33;
Matches 135; Conservative 0; Mismatches 1; Indels

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317	ACAACCAGAGCGAGGTGGTCTCACA	CCTCCAGGAAATGAATGGCTCGCATGGGCG	376
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61	ACAACCAGAGCGAGGTGGTCTCACA	CCTCCAGGAAATGAATGGCTCGCATGGGCG	120
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121	CCGACGGACGCCTCCT	136	
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RESULT 15
US-10-242-535A-33425
/ Sequence 33425, Application US/10242535A
/ Publication No. US20040013663A1
/ GENERAL INFORMATION:
/ APPLICANT: ChondroGene Inc.
/ APPLICANT: Liaw, C.C.
/ TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
/ FILE REFERENCE: 4231/2005
/ CURRENT APPLICATION NUMBER: US/10/242,535A
/ CURRENT FILING DATE: 2002-09-12
/ PRIOR APPLICATION NUMBER: US 10/085,783
/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/305,340
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/275,017
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 33425
/ LENGTH: 217
/ TYPE: DNA
/ ORGANISM: Human
US-10-242-535A-33425

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Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 81; Conservative 0; Mismatches 0; Indels
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 QY 1017 GAGCTACTCTCAGGCTGCAGT 1037
 Db 78 GAGCTACTCTCAGGCTGCAGT 98

Search completed: December 16, 2004, 17:19:21
 Job time : 675 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using gw model

Run on: December 16, 2004, 12:47:28 ; Search time 4075 Seconds

(without alignments)

9738.127 Million cell updates/sec

Title: US-09-819-371-1

Perfect score: 1089

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Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 3282875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hlc:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	681	62.5	896	5	BQ588194
5	654	60.1	1130	4	BM917072
6	652	59.9	949	4	BM561951
7	649	59.6	928	5	BQ710481
8	642	59.0	718	4	BG679105
9	635	58.3	875	5	BQ962778
10	630	57.9	931	5	BQ926296
11	614	56.4	892	5	BQ690438
12	613	56.3	790	1	AV752612
13	611	56.1	645	2	BF975616
14	610	56.0	636	2	BF725277
15	609	55.9	612	6	CA391513
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20	582	53.4	852	4	BM923524
21	567	52.1	941	5	BQ711764
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23	551	51.1	705	6	CB529818
24	557	51.1	708	6	CB528498

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	27	537	49.3	618	4	BM842679	K-EST0120
C	28	536	49.2	721	6	CD367343	UI-H-FT2-
	29	533	48.9	590	4	BG831090	60276640
	30	529	48.6	933	4	BM456332	AGENCOURT
	31	528	48.5	590	4	BG767374	602741158
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	33	524	48.1	699	6	CB529146	UI-H-FT2-
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	36	501	46.0	692	6	CA308900	UI-H-FT1-
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DEFINITION AGENCOURT_14394444 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30408575 5', mRNA sequence.
CD514705
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
GI:31446423
Homo sapiens (human)

REFERENCE
1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/
TITLE
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Blgg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: NDAM491 row: 1 column: 24
High quality sequence stop: 680.
Location/Qualifiers
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/tissue_type="White Matter"
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/clone_lib="NIH_MGC_181"
/note="vector: pCMV-SPT6.1; Site 1: NotI; Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

FEATURES

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ORIGIN

CD514705
AGENCOURT_14394444 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30408575 5', mRNA sequence.
CD514705
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
GI:31446423
Homo sapiens (human)

639	QY	CCCAATCTCTGACCATGAGGCCACCTCTGAGGTGCTGGGCCCTTCTACCTTCGCGA	638
638	Db	CCCAATCTCTGACCATGAGGCCACCTCTGAGGTGCTGGGCCCTTCTACCTTCGCGA	697
699	QY	GATCAGCGTGACCTGGCAGCGGGATGGGGAGGACACAGCCAGGACACAGAGCTTGTGGA	758
698	Db	GATCAGCGTGACCTGGCAGCGGGATGGGGAGGACACAGCCAGGACACAGAGCTTGTGGA	757
759	QY	GACCAGGCGCTGACGGGGATGGAACTTTCAGAACTGG	795
758	Db	GACCAGGCGCTGACGGGGATGGAACTTTCAGAACTGG	794

RESULT 3
CD512828
LOCUS
DEFINITION
CD512828 897 bp mRNA linear EST 06-JUN-2003
AGENCOURT 14373093 NIH MGC 179 Homo sapiens CDNA clone
IMAGE:30394728 5' mRNA sequence.

CDS12828.1 GI:31444345
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 897)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Daniela S. Gerbard, Ph.D.

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM473 row: 1 column: 01
High quality sequence start: 8
High quality sequence stop: 707.

ORIGIN

RESULT 4
 BQ688194
 LOCUS
 DEFINITION
 BQ688194
 AGNCOURT_8064678 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206180
 5', mRNA sequence.
 BQ688194
 BQ688194.1 GI:21813510
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 886)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue Procurement: ATCC

	Query Match	Best Local Similarity	64.6%	Score 703;	DB 6;	Length 897;
	Matches 703;	Conservative	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	334	GGGTCTCACACCTCCAGGGAAATGAATGGCTGCGACATGGGCCCGACGAGCGCTCTCTC	393			
Db	43	GGGTCTCACACCTCCAGGGAAATGAATGGCTGCGACATGGGCCCGACGAGCGCTCTCTC	102			
QY	394	CGCGGGTATCACCGACGCGCTACGACGGCAAGGATTACATCTCCCTGAACGAGGACCTG	453			
Db	103	CGCGGGTATCACCGACGCGCTACGACGGCAAGGATTACATCTCCCTGAACGAGGACCTG	162			


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Db 429 GCAAGGATTACATCTCCCTGAAGAGGACCTGGCTCTGGAGCCGGCGGACACCGTG 488
QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGAGGAGTTTCAGGACCTAC 540
Db 489 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGAGGAGTTTCAGGACCTAC 548
QY 541 CTGAGGGCGAGTGCTCGAGTCTCTCGAGATCTTGGAGATGAGGATGGAGAGGAGCGCTA 600
Db 549 CTGAGGGCGAGTGCTCGAGTCTCTCGAGATCTTGGAGATGAGGATGGAGAGGAGCGCTA 608
QY 601 CAGCGCGAGATCTCTCCAAAGGACACAGTTCCCAACCAACCCCATCTCTGACCAT 654
Db 609 CAGCGCGAGATCTCTCCAAAGGACACAGTTCCCAACCAACCCCATCTCTGACCAT 662

RESULT 6
BM561951 349 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT_6593172 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5484505
5', mRNA sequence.
ACCESSION BM561951
VERSION 1
KEYWORDS 1 (bases 1 to 949)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2013 row: o column: 02
High quality sequence stop: 682.
Location/Qualifiers
1..949
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/mol_type="mRNA"
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/clone="IMAGE:5484505"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_106"
/notes="Organ: blood; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
source
Query Match 59.9%; Score 652; DB 4; Length 949;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGCGCCGAGAGCTCTCTGCTCTCAGGGCCCTGCGCTGACCGGATATTGG 60
Db 27 ATGGGCGCCGAGAGCTCTCTGCTCTCAGGGCCCTGCGCTGACCGGATATTGG 86
QY 61 GCGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGGGGCCCGCGGGAG 120
Db 87 GCAGGCTCCCACTCTCTGAGTATTTCAGCACCGCTGTGTGGGGCCCGCGGGAG 146

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QY 121 CCCCGCTACATCGCCGCTGGAGTACGTAGACGACACACCAATTCCTCGGTTCCAGACGAC 180
Db 147 CCCCGCTACATCGCCGCTGGAGTACGTAGACGACACCAATTCCTCGGTTCCAGACGAC 206
QY 181 GCGCGGATTCGAGGATGAGAGCGCGGAGCGGCTGGTGGTGGAGCAAGAGGGCGCGAGTAT 240
Db 207 GCGCGGATTCGAGGATGAGAGCGCGGAGCGGCTGGTGGTGGAGCAAGAGGGCGCGAGTAT 266
QY 241 TGGAGTGGGACCAACAGGGTATCGCAAGGCGCAACGCAAGAGTGGAGTGGCGCTGAGG 300
Db 267 TGGAGTGGGACCAACAGGGTATCGCAAGGCGCAACGCAAGAGTGGAGTGGCGCTGAGG 326
QY 301 AACCTGTCTCGCGCTACAAACAGAGAGGAGGCTGGTCTCACACCTCCAGAGGAATGAAT 360
Db 327 AACCTGTCTCGCGCTACAAACAGAGAGGAGGCTGGTCTCACACCTCCAGAGGAATGAAT 386
QY 361 GCGTGGACATGAGGGGCGCGAGCGGCTCTCCGCGGGTATCACAGACGCGGTACGAC 420
Db 387 GCGTGGACATGAGGGGCGCGAGCGGCTCTCCGCGGGTATCACAGACGCGGTACGAC 446
QY 421 GCGAAGGATTACATCTCCCTGAAACAGGAGACCTCGGCTCTGGAGCGCGGCGACACCGTG 480
Db 447 GCGAAGGATTACATCTCCCTGAAACAGGAGACCTCGGCTCTGGAGCGCGGCGACACCGTG 506
QY 481 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGAGTTCAGGACCTAC 540
Db 507 GCTCAGATCACCCAGCGCTTCTATGAGCGAGAGGAATATGACAGAGTTCAGGACCTAC 566
QY 541 CTGAGGCGGAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGGAAGAGAGCGCTA 600
Db 567 CTGAGGCGGAGTGCCTGGAGTTGCTCCGAGATCTTGGAGATGGGAAGAGAGCGCTA 626
QY 601 CAGCGCGAGATCTCTCCAAAGGACACAGTTGCCACACCCCATCTCTGACCATGAGGC 660
Db 627 CAGCGCGAGATCTCTCCAAAGGACACAGTTGCCACACCCCATCTCTGACCATGAGGC 686
QY 661 ACCCTGAGTGTCTGGGCGCTTCTACCTCGGAGATACGCTGACCTGGCAGCGG 720
Db 687 ACCCTGAGTGTCTGGGCGCTTCTACCTCGGAGATACGCTGACCTGGCAGCGG 746
QY 721 GATGGGAGGAACAGACCCAGGACAGAGCTTG 754
Db 747 GATGGGAGGAACAGACCCAGGACAGAGCTTG 780

RESULT 7
BM710481 928 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8353524 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279516
5', mRNA sequence.
ACCESSION BM710481
VERSION 1
KEYWORDS 1 (bases 1 to 928)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: d column: 13
High quality sequence stop: 647.

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Db      436 GCAGGATACATCCCTGACGAGGACCTGCGCTCTGACCGCGGCGACACCGTG 495
Qy      482 CTGAGTACCCAGCGCTTCTATGAGGAGAGGAGATATGACAGAGGTTGAGGACCTACC 541
Db      496 CTGAGTACCCAGCGCTTCTATGAGGAGAGGAGATATGACAGAGGTTGAGGACCTACC 555
Qy      542 TGAGGCGGAGTGCCTCGGAGTTCCTCCGAGATATCTGGAGATGGGAAGGAGACGCTAC 601
Db      556 TGAGGCGGAGTGCCTCGGAGTTCCTCCGAGATATCTGGAGATGGGAAGGAGACGCTAC 615
Qy      602 AGCGCGAGATCTCCAAAGGACACGTTGCCACCCACCCATCTTGCACATGAGGCCA 661
Db      616 AGCGCGAGATCTCCAAAGGACACGTTGCCACCCACCCATCTTGCACATGAGGCCA 675
Qy      662 CCCTGAGTGCCTGGGCGCTTCTACCTTCGCGAGATCA 703
Db      676 CCCTGAGTGCCTGGGCGCTTCTACCTTCGCGAGATCA 717

RESULT 9
BO962778
LOCUS
DEFINITION
BO962778 875 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8820719 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:6380038
5', mRNA sequence.
BO962778
VERSION
BO962778.1 GI:22378256
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2567 row: p column: 23
High quality sequence stop: 673.
Location/Qualifiers
1..875
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/db_xref="taxon:9606"
/clone="IMAGE:6380038"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 58.3%; Score 635; DB 5; Length 875;
Best Local Similarity 99.6%; Pred. No. 5.1e-307;
Matches 785; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ATGGCGCGGAGCTCTCTGCTCTCAGGGCGCTGGCGCTGACCGATCTTGG 60

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Db      4 ATGGCGCGGAGCTCTCTGCTCTCAGGGCGCTGGCGCTGACCGATCTTGG 63
Qy      61 CGGGCTCCACCTCTTGGAGTATTTACGACCGCTGTCTCGGGCGCGCGGGAG 120
Db      64 CGAGGCTCCACCTCTTGGAGTATTTACGACCGCTGTCTCGGGCGCGCGGGAG 123
Qy      121 CCCGCTACATCGCGCTGGAGTACGTAGACGACACCAATTTCTGCGGTTGACAGCGAC 180
Db      124 CCCGCTACATCGCGCTGGAGTACGTAGACGACACCAATTTCTGCGGTTGACAGCGAC 183
Qy      181 GCCCGGATTCGAGGATGGAGCGCGGAGCGGTGGTGGAGCAGAGAGGGCGGAGTAT 240
Db      184 GCCCGGATTCGAGGATGGAGCGCGGAGCGGTGGTGGAGCAGAGAGGGCGGAGTAT 243
Qy      241 TGGAGTGGACCAACAGGTTACGCCAAGGCCAACCGCACAGACTGACCGAGTCCCTGAGG 300
Db      244 TGGAGTGGACCAACAGGTTACGCCAAGGCCAACCGCACAGACTGACCGAGTCCCTGAGG 303
Qy      301 AACCTGCTCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCTCAGAGGAATGAAT 360
Db      304 AACCTGCTCGCGCTACAAACAGAGGAGGCTGGGTCTCACACCTCTCAGAGGAATGAAT 363
Qy      361 GGCTGGACATGGGGCGCGGACGCGCTCTCCGCGGGTATCACAGACACGCTACGAC 420
Db      364 GGCTGGACATGGGGCGCGGACGCGCTCTCCGCGGGTATCACAGACACGCTACGAC 423
Qy      421 GGCAAGGATTACATCTCCCTGAAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTG 480
Db      424 GGCAAGGATTACATCTCCCTGAAACGAGGACCTCGCTCTCGGACCGCGCGGACACCGTG 483
Qy      481 GCTCAGATCACCGAGCGCTTCTATGAGGACAGAGGAATATGACAGAGTTTACGACCTTAC 540
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Qy      541 CTGAGGCGGAGTGCCTGGAGTTGCTCCGAGATATCTGGAGATGGGAAGGAGACGCTA 600
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Qy      601 CAGCGCGAGATCTCCAAAGGACACAGTTGCCACACCCATCTCTGACCATGAGGCC 660
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Qy      661 ACCCTGAGGTGCTGGGCGCTTCTACCTTCGCGAGATCACGCTGCGGAGATCACGCTGCGAGCGG 720
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Qy      721 GATGGAGGACAGACCCAGGACACAGCTTGTGGACACCGCTCTCAGGGGATGGA 780
Db      724 GATGGAGGACAGACCCAGGACACAGCTTGTGGAGACCGGCTCTGAGGGGATGGA 783
Qy      781 ACCTTCCA 788
Db      784 ACCTTCCA 791

RESULT 10
BO926296
LOCUS
DEFINITION
BO926296 931 bp mRNA linear EST 20-AUG-2002
AGENCOURT_8826885 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6424309
5', mRNA sequence.
BO926296
VERSION
BO926296.1 GI:22341327
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

```

Tissue Procurement: DCTD/DTP/Gadgar
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM2604 row: e column: 14
 High quality sequence stop: 638.

FEATURES

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 /clone_lib="NIH_MGC_18"
 /note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.9%; Score 630; DB 5; Length 931;
 Best Local Similarity 99.9%; Pred. No. 1.6e-304;
 Matches 680; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGCCGAGCCTCTCTGCTCTCTAGGGCCCTGCTGACCGATCTGG 60
 DB 15 ATGGGCGCCGAGCCTCTCTGCTCTCTAGGGCCCTGCTGACCGATCTGG 74
 QY 61 GCGGCTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGCGCGCGGGAG 120
 DB 75 GCGGCTCCCACTCTTGGATATTTCAGCACCGCTGTGTGCGGCGCGCGGGAG 134
 QY 121 CCCGCTACATCGCGTGGAGTACTAGACGACGCAATTCCTGGGTTCGACGCGAC 180
 DB 135 CCCGCTACATCGCGTGGAGTACTAGACGACGCAATTCCTGGGTTCGACGCGAC 194
 QY 181 GCGCGATTCCAGGATGGAGCCGCGGAGCGCTGTGGGTGAGCAAGAGGGCGGAGTAT 240
 DB 195 GCGCGATTCCAGGATGGAGCCGCGGAGCGCTGTGGGTGAGCAAGAGGGCGGAGTAT 254
 QY 241 TGGGAGTGACACAGGATAGCCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGG 300
 DB 255 TGGGAGTGACACAGGATAGCCCAAGGCCAACGACAGACTGACCGAGTGGCCCTGAGG 314
 QY 301 AACCTGCTCCGCGCTACACAGAGCGAGGCTGGGTCTCACACCTTCAGGGAATGAAT 360
 DB 315 AACCTGCTCCGCGCTACACAGAGCGAGGCTGGGTCTCACACCTTCAGGGAATGAAT 374
 QY 361 GCTGCGACATGGGGCCCGGAGCGAGCGCTCTCTCGGGGTATCACCAGCAGCGTACGAC 420
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 QY 421 GCGAGGATACATCTCCCTGAACGAGGACTCGCTCTGGAGCGCGCGGACCGGTG 480
 DB 435 GCGAGGATACATCTCCCTGAACGAGGACTCGCTCTGGAGCGCGCGGACCGGTG 494
 QY 481 GCTCAGATCACCCAGCGCTTCTATGAGGAGAGGAAATATGACAGGAGTTTACGACCTAC 540
 DB 495 GCTCAGATCACCCAGCGCTTCTATGAGGAGAGGAAATATGACAGGAGTTTACGACCTAC 554
 QY 541 CTGGAGGCGAGTGGCTGGAGTCTCCGCGAGTACTTGGAGATGGGAGGAGCGCTA 600
 DB 555 CTGGAGGCGAGTGGCTGGAGTCTCCGCGAGTACTTGGAGATGGGAGGAGCGCTA 614
 QY 601 CAGCGCGCAGATCTCTCCAAAGGACACAGTTGTGCCCAACACCCCTCTCTGACCATGAGGCC 660

Db 615 CAGCGCGCAGATCTCTCCNAAGGCACACGTTGCCACCCCATCTCTGACCATGAGGCC 674
 QY 661 ACCCTGAGGTGCTGGGCCCTG 681
 Db 675 ACCCTGAGGTGCTGGGCCCTG 695

RESULT 11

BQ690438 892 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT_8343876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248481
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ690438
 VERSION BQ690438.1 GI:21815754
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 892)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1995).
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM2388 row: g column: 10
 High quality sequence stop: 623.

FEATURES

Location/Qualifiers
 1..892
 /organism="Homo sapiens"
 /mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="IMAGE:6248481"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 56.4%; Score 614; DB 5; Length 892;
 Best Local Similarity 99.8%; Pred. No. 1.8e-296;
 Matches 664; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGCGCCCGAGCGCTCTCTGCTCTCTAGGGCCCTGCGCCCTGACCGATCTGG 61
 DB 1 TGGCGCCCGAGCGCTCTCTGCTCTCTAGGGCCCTGCGCCCTGACCGATCTGG 60
 QY 62 CGGGCTCCCACTCTTGGAGTATTTCAGCACCGCTGTGTGCGGCGCGCGGGAGC 121
 DB 61 CAGGCTCCCACTCTTGGAGTATTTCAGCACCGCTGTGTGCGGCGCGCGGGAGC 120
 QY 122 CCGGCTACATCGCGCTGGAGTACGTAGACGACGCAATTCCTGCGGTTTCAGCGGAGC 181
 DB 121 CCGGCTACATCGCGCTGGAGTACGTAGACGACGCAATTCCTGCGGTTTCAGCGGAGC 180
 QY 182 CCGGATTCGAGGATAGAGCGCGGAGCGCGTGGGTGGAGGAGGCGCGGAGTAT 241
 DB 181 CCGGATTCGAGGATAGAGCGCGGAGCGCGTGGGTGGAGGAGGCGCGGAGTAT 240

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
<http://image.llnl.gov>
 Plate: L1CM210 row: d column: 19
 High quality sequence start: 645.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone_image="4336866"
 /tissue_type="primary B-cells from tonsils. (cell line)"
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 /note="Organ: B-cells; Vector: pOT87; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 56.1%; Score 611; DB 2; Length 645;
 Best Local Similarity 100.0%; Pred. No. 5.7e-295;
 Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

427 GATTACATCTCCCTGACGAGGACCTCGCTCTGACCGCGCGGACACCGCTGCTCAG 486
 Db 1 GATTACATCTCCCTGACGAGGACCTCGCTCTGACCGCGCGGACACCGCTGCTCAG 60
 QY 487 ATCACCAGCGCTTCTATGAGGAGAGGATATGCGAGGAGTTCAGGACCTACCTGGAG 546
 Db 61 ATCACCAGCGCTTCTATGAGGAGAGGATATGCGAGGAGTTCAGGACCTACCTGGAG 120
 QY 547 GCGAGTGCTGGAGTTCCTCCGACATCTTGGAGATGGGAAGGACGCTACAGCGC 606
 Db 121 GCGAGTGCTGGAGTTCCTCCGACATCTTGGAGATGGGAAGGACGCTACAGCGC 180
 QY 607 GCAGATCTCCAAAGGACACGCTGCGCCACCCCATCTCTGACCATGAGCCACCTG 666
 Db 181 GCAGATCTCCAAAGGACACGCTGCGCCACCCCATCTCTGACCATGAGCCACCTG 240
 QY 667 AGGTGCTGGGCGCTTCTACCTGCGAGATCACGCTGACCTGGCGAGGATGGG 726
 Db 241 AGGTGCTGGGCGCTTCTACCTGCGAGATCACGCTGACCTGGCGAGGATGGG 300
 QY 727 GAGGAACAGACCCAGGACACGAGCTTGGAGACAGGACCGCTGAGGGATGGACCTTC 786
 Db 301 GAGGAACAGACCCAGGACACGAGCTTGGAGACAGGACCGCTGAGGGATGGACCTTC 360
 QY 787 CAGAAGTGGGCGCTGTGTGTGTGCTTCTGGAGAGGAACAGAGATACATGSCCATGTG 846
 Db 361 CAGAAGTGGGCGCTGTGTGTGTGCTTCTGGAGAGGAACAGAGATACATGSCCATGTG 420
 QY 847 CAGCAGAGGGGCTGCGCCAGCCCTCATCTGAGATGGAGGAGTCTCCCGAGCCAC 906
 Db 421 CAGCAGAGGGGCTGCGCCAGCCCTCATCTGAGATGGAGGAGTCTCCCGAGCCAC 480
 QY 907 ATCCCCATCGTGGGACATGTTGTGTGCTTGTGCTTGTGAGCTGTGTGCTACCTGAGCT 966
 Db 481 ATCCCCATCGTGGGACATGTTGTGTGCTTGTGCTTGTGAGCTGTGTGCTACCTGAGCT 540
 QY 967 GTGCTGCTGCTGTGTGTGTGAGGAGAGAGCTCAGATAGAAACAGAGGAGCTACTCT 1026
 Db 541 GTGCTGCTGCTGTGTGTGTGAGGAGAGAGCTCAGATAGAAACAGAGGAGCTACTCT 600
 QY 1027 CAGGCTGCAGT 1037
 Db 601 CAGGCTGCAGT 611

RESULT 14

Bf725277 636 bp mRNA linear EST 05-JAN-2001
 LOCUS bxl14a11.y1 Human Iris cDNA (Un-normalized, unamplified): EX Homo
 DEFINITION sapiens cDNA clone bxl14a11 5', mRNA sequence.

ACCESSION Bf725277
 VERSION Bf725277.1 GI:12041188
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 636)
 Wistow G.J., Bernstein S., Behal A. and Smith D.
 NEIBANK: EST analysis and bioinformatics for ocular genomics
 Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 CONTACT: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graceme@helix.nih.gov

Plate: 14 row: a column: 11
 Seq primer: M3RPI reverse primer (ABI).
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bxl14a11"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
 EX"

NOTE="Organ: Eye; Vector: pCMVSPORT6, Post-mortem iris
 tissue was pooled from 10 individuals ranging in age from
 4-80 years and RNA was extracted. From this pooled sample
 an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
 directionally cloned cDNA library in the pCMVSPORT6 vector
 was constructed at Life Technologies, essentially
 following the protocols of the Superscript Plasmid System
 full details of which are contained in the manufacturer's
 instruction manual (<http://www.lifetech.com/>). First
 strand synthesis was carried out using a Not I
 primer-adaptor
 [5'-PGACTAGTCTAGATCGGCGCGCC(T)15-3']. Not I/blunt
 end inserts were cloned into the Not I/BcoR V sites in the
 vector. EST analysis was performed on the unamplified
 library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 56.0%; Score 610; DB 2; Length 636;
 Best Local Similarity 100.0%; Pred. No. 1.8e-294;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCGCCCGGAGGCTCTCTGCTCTCAGGGCCCTGGCCCTGACGATCTTGG 60
 Db 27 ATGGCGCCCGGAGGCTCTCTGCTCTCAGGGCCCTGGCCCTGACGATCTTGG 86
 QY 61 GGGGGCTCCCACTCTCTGAGGTATTTAGCACCGCTGTGCGCGCCCGCGGGGAG 120
 Db 87 GGGGGCTCCCACTCTCTGAGGTATTTAGCACCGCTGTGCGCGCCCGCGGGGAG 146
 QY 121 CCGCGCTACATCGCGTGGAGTACAGACACGCAATCTCGGTTGACAGCGAC 180
 Db 147 CCGCGCTACATCGCGTGGAGTACAGACACGCAATCTCGGTTGACAGCGAC 206
 QY 181 GCGCGATTCCGAGGATGGAGCCGCGGAGCGCTGGGTGGAGCAAGAGGGCGGCTAT 240

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